Cellulose binding
Clostridium cellul
Gaussia luciferase
Gaussia luciferase
Gaussia species CB
C. cellulovorans C
C. cellulovorans C
C. cellulose binding
A mannanase-linker

Clostridium cellul

Pectate lyase-link Pectate lyase CBD Scaffoldin protein C. thermocellum ce Truncated cellulas

Active cellulase h Truncated cellulas Active cellulase p Pseudomonas aerugi

Active cellulase p Truncated cellulas

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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1..95
/label= Undefined_N-terminal_fusion_partner
/label= C17E2_OspA
/note= "Product of OspA gene optimised for expression in
Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C17E2 OspA construct with N-terminal fusion partner.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                       AAE16325
AAY13493
ABJ18820
ABJ18820
AAG63962
AAG63963
AAG63963
AAG63963
AAG63963
ABP71658
ABP73029
ABP73020
ABP73020
ABP73020
                                                                             AAW90081
AAR95080
AAY24123
AAY28850
AAY43218
AAW1523
AAW13108
AAW13108
AAW13492
AAW13492
                                                      AAE13383
AAW90077
                                AAE05748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB81128 standard; Protein; 256 AA
 99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piscirickettsia salmonis.
Synthetic.
CA2281913-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1999;
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120.5
120.5
115
115
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483
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480.5
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Region
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 E. coll codon opti
Optimised Ospa pro
Escherichia coll c
Piscirickettsia sa
Ospa antigen amino
Piscirickettsia sa
Clostridium cellul
Chimeric S peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C17E2 OspA constru
                                                                          November 5, 2003, 20:06:21; Search time 46.4249 Seconds (without alignments) 875.264 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                A_Geneseq_19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqfy-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqfy-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseqfy-embl/AA1983.DAT:*
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| SIDSI/gcgdata/geneseqfy-embl/AA2003.DAT:*
| SIDSI/gcgdata/geneseqfy-embl/AA2003.DAT:*
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1335
1 MSVEFYNSNKSAQTNSITPI......IYGTACPQPDGRWQVISTEK 256
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          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                       1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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AAU97869
AAB81127
AAU97868
AAG78025
AAG78025
AAB057867
AAE05746
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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256
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162
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328
                    Copyright
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Match
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100.0
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62.3
61.0
61.0
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99CA-2281913

17-SEP-1999;

1335 1335 832 832 815 815 815 487

Result Š.

Amino acid sequenc Amino acid sequenc A. cellulolyticus A. cellulolyticus Corrected Bacillus Amino acid sequenc Protein encoded by Brotein encoded by

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RESULT 3
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                                                                                                                                                                                               This invention relates to a method for the protection against infection of a poixlothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed 05pA, or an immunogenic fragment of 05pA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a P. salmonis OspA construct optimised for expression in Escherichia coli, fused to an undefined N-terminal fusion partner. The fusion protein is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGNSYVDNTSKVTANFVKETASPTSTYDDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
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                                                                                                                       Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKVKAGQVTRWRNPDJGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKVKAGGVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVEPYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer suxface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease; 17e2.
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0
                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 1335; DB 22; Length 256; Local Similarity 100.0%; Pred. No. 9.1e-123; les 256; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU97869 standard; Protein; 256 AA.
                                                                                                                                                                          Example 4; Fig 5; 35pp; English
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                                                            Kuzyk MA
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                                                                                  WPI; 2001-316844/34.
N-PSDB; AAF86248.
                                                            Burian J,
                                   KUZYK M A.
                       BURIAN J
          KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                      (BURI/)
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                                                          Kay WW,
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Matches
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The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprocein), its variants, non-lipidated form or antigenic peptides derived or.synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related respectively in fin-fish against Rickettsial septicaemia and other related. This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) with an N-terminal fusion used in the creation of the vaccine described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
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100.0%; Pred. No. 9.1e-123;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       Kuzyk MA;
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                                                                                                                      19-MAR-2001; 2001CA-2339327.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strain, as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-455221/49.
                                                                                                                                                                                                                                                (THOR/) THORNTON J
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                                                                                                                                                                                                                                                                          (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 AA;
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CA2339327-A1
                                                         15-MAR-2002
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Synthetic

Region

Key

Kay WW,

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The invention describes a method of protecting a polkilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of form or infinitish against Rickettsial septicaemia and other related Rickettsial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) used in the creation of the vaccine described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LGGLIGSKIGQSMDQQDXIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
                                                                                                       Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease; 17e2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.3%; Score 832; DB 23;
100.0%; Pred. No. 1.4e-73;
iive 0; Mismatches 0;
                                                                 Escherichia coli codon optimised OspA, 17e2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burian J,
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                                                                                                                                                                                                                                                                                                                                                                       19-MAR-2001; 2001CA-2339327.
                                                                                                                                                                                                                                                                                                                                                                                                                  15-SEP-2000; 2000US-0677374.
                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 161; Conservative
                                                                                                                                                                                                          Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kay ww,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (THOR/) THORNTON J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain, as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-455221/49.
N-PSDB; ABK52402.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thornton JC,
                                                                                                                                                                                                                                                                           CA2339327-A1.
                     12-AUG-2002
                                                                                                                                                                                                                                                                                                                         15-MAR-2002.
                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KAYW/)
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ID AAG7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a method for the protection against infection of a poixlothermic fish by the bacterial pathogen, Piscirckettsia asalmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed 08pA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkliothermic fish, against the bacterial pathogen P. Salmonis. The method is also useful for protecting against salmonis rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents optimised P. salmonis OspA protein 1782. The DNA encoding OspA 1782 (AAF86247) has been optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
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                                        Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 RRÓGYCREFGGKAMIAGGKGEIYGTACPOPDGRWQVISTEK 161
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Optimised OspA protein 17E2 amino acid sequence
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Matches 161; Conservative 0; Mismatches
                                                                                                                                                                                                                                109..128
/label= B_cell_epitope
                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                          99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                          99CA-2281913
                                                                                                                                       Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-316844/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAF86247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAYW/) KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-1999;
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Gaps

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Length 161; Indels

Seguence Query Match

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AAU97868

AAU97868 ID AAU9 XX

RESULT 4

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215

AAG78025

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This invention relates to a method for the protection against infection of a poixilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA, in the form of a vaccine. The method is used for protecting animals, particularly poixilothermic fish, against the bacterial pathogen p. salmonis. The method useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents P. salmonis OspA protein. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROOYCREFOOKAMIAGOKOEIYGTACPOPDGRWOVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 815; DB 22;
Pred. No. 6.4e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                            110..129
/label= B_cell_epitope
                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU97867 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 2B; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                      Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.0%;
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                                                     salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                          2001-316844/34
                                                                                                                                                                                                                                                                                                                                                                                      Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                            (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAF86246
                                                       Piscirickettsia
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                                                                                                                                                                                                                                         17-SEP-1999;
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                                                                                                                                                                 CA2281913-A1
                                                                                                                                                                                                     17-MAR-2001
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                                                                                           Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 RGCLÓGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acid sequences and the encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity to protect fish against P. salmonis which causes piscirickettsiosis, also known as salmonid rickettsial septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen;
                                                                                           Piscirickettsia salmonis; piscirickettsiosis; salmonid rickettsial; septicaemia; SRS; surface antigen; vaccine; antibacterial; fish; ATCC VR-1361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids encoding an amino acid sequence homologous to the surface antigen present on Piscirickettsia salmonis are useful to protect fish against piscirickettsiosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valenzuela P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 815; DB 22;
Pred. No. 6.4e-72;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Griffiths S,
                                                                          Piscirickettsia salmonis polypeptide P10.6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                  2000GB-0016080.
2000GB-0016082.
2000GB-0018599.
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98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                          (AQUA-) AQUA HEALTH EURO LTD
                                                                                                                                                                                                                                                                                            12-MAR-2001; 2001WO-GB01055
                                                                                                                                                                                                                                                                                                                                  2000GB-0005838
                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.8
Matches 158; Conservative
                                                                                                                                                                                    Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ı,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brouwers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-639050/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH79040.
                                                                                                                                                                                                                      WO200168865-A2
                                                                                                                                                                                                                                                                                                                                                  01-JUL-2000;
01-JUL-2000;
29-JUL-2000;
                                                                                                                                                                                                                                                                                                                                  11-MAR-2000;
                                     15-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simard N,
Burzio L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217
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Sequence

Query Match

AAB81126 RESULT

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The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.
The method involves treating the polysaccharide structure with a
polysaccharide binding domain (PBD) fusion protein. The method is
used to alter the structural, chemical, physical, electrical and
mechanical properties of polysaccharide materials such as paper,
yarns, fibers and textiles, using biological crosslinking agents.
The polysaccharide containing materials have improved mechanical
properties such as wet strengths, durability and elasticity. The PBD
reagent is applied in the forming steep in fluting paper manufacture
which eliminates the sizing steep. The use of a biological crosslinker
improves the recyclability of paper products. The PBD reagent maintains
the fine fibers in a slurry therefore resulting in better recovery of
raw materials. The PBD molecules are eluted by strong alkaline conditions
which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP------KVTGYIGGAK--VL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
  Polysaccharide modification; polysaccharide binding domain; PBD; paper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present requence is Clostridium cellulovorans cellulose binding domain (CBD)-180. CBD-180 contains 180 amino acids of C. cellulovorans CBD (CBDclos) of cellulose binding protein A (CBP A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------KKGOFITIO----
                  yarn; fiber, textile, biological crosslinker; mechanical property; Clostridium cellulovorans cellulose binding domain; wet strength; durability; elasticity; CBDclos; cellulose binding protein A; CBP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.5%; Score 487; DB 22;
46.8%; Pred. No. 1.4e-39;
ative 12; Mismatches 30;
                                                                                                                                                                                                                                                                                                                               (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1.2; Fig 1e-1g; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                            Shoseyov 0;
                                                                                                                                                                                                                                                                        99US-0164140.
                                                                                                                                                                                                                                  02-NOV-2000; 2000WO-IL00708
                                                                                                                 Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Nussinovitch A,
                                                                                                                                                                                                                                                                                                                                                                                                                                2001-457121/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           penetrate paper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD11043
                                                                                                                                                       WO200134091-A2
                                                                                                                                                                                                                                                                        08-NOV-1999;
                                                                                                                                                                                                                                                                                             18-NOV-1999;
                                                                                                                                                                                              17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                            Levy I,
  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain piscirickettsia salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related Rickettsial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Piscirickettsia salmonis outer surface lipoprotein, OspA, used in the creation of the vaccine described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RGCLÓGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium cellulovorans cellulose binding domain-180 (CBD-180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 ROQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQQYCREFQQKAMIAGQKQBIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 815; DB 23;
Pred. No. 6.4e-72;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                          Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE05746 standard; Protein; 190 AA
                                                                                                                                                                                                                                                                                                                                                                          Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.0%;
98.8%;
                                                                                                                                                                                            19-MAR-2001; 2001CA-2339327
                                                                                                                                                                                                                                  15-SEP-2000; 2000US-0677374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 98.8
nes 158; Conservative
                                                                            Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                      Thornton JC, Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strain, as a vaccine
                                      Rickettisial disease.
                                                                                                                                                                                                                                                                        (THOR/) THORNTON J C.
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-455221/49.
                                                                                                                                                                                                                                                                                           KAY W W.
BURIAN J.
KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABK52401.
                                                                                                                 CA2339327-A1
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                                                                                                                                                       15-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE05746;
                                                                                                                                                                                                                                                                                           (KAYW/) F
(BURI/) E
(KUZY/) F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE05747;
                                                                                                            Seguence
                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                       127
                                                                                                                                                                                                                                                                                                                                                      146
                                                                                                                                                                                                                                                                                                                                                                              239
                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levy I,
 which
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials. The method involves treating the polysaccharide structure with a
polysaccharide binding domain (PBD) fusion protein. The method is
used to alter the structural, chemical, physical, electrical and
mechanical properties of polysaccharide materials such as paper,
yarns, fibers and textiles, using biological crosslinking agents.
The polysaccharide containing materials have improved mechanical
properties such as wet strengths, durability and elasticity. The PBD
reagent is applied in the forming stage in fluting paper manufacture
which eliminates the sizing step. The use of a biological crosslinker
improves the recyclability of paper products. The PBD reagent maintains
the fine fibers in a slurry therefore resulting in better recovery of
raw materials. The PBD molecules are eluted by strong alkaline conditions
                                                                                                                                                                                                                                                                                                                                                               /label= Unknown
/note= "Encoded by TAG"
327...38
/note= "These residues are absent in the sequence shown
as SEQ ID NO: 10 in the sequence listing"
                                                                                                                                                                                  Polysaccharide modification; polysaccharide binding domain; PBD; paper;
                                                                                                                                                                                                                                                                                                       30..208
/note= "This region is derived from C. cellulovorans"
                                                                                                                                                                                              yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; cellulose binding domain; CBD; chimeric protein; S peptide-cellulose binding domain-S protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparation of a polysaccharide containing material having at least desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                              226..326
/note= "This region is derived from bovine"
                                                                                                                                                          Chimeric S peptide-cellulose binding domain-S protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoseyov 0;
                                                                                                                                                                                                                                                      Chimeric - Clostridium cellulovorans Chimeric - Bos sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Fig 4b-4g; 121pp; English
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                   AAE05749 standard; Protein; 328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0164140.
99US-0166389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-2000; 2000WO-IL00708.
                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levy I, Nussinovitch A,
                                                                                                                                                                                                                                  Spep-CBD-Sprot; bovine
 GTACPQPD 246
                       154 ĠTA-PGPD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-457121/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD11046
                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200134091-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-1999;
                                                                                                                                  24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-2001
                                                                                                          AAE05749;
 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         property
                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                               Region
                                                                       AAE05749
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The present sequence is S peptide-cellulose binding domain-S protein (Spep-CBD-Sprot), a fusion protein derived from Clostridium cellulovorans and bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP------KVTGYIGGAK--VL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; cellulose binding domain; CBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------KKĠÒFITIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "This residue is absent in the sequence shown
                                                                                                                                                               Note: This sequence is stated to be the same as that shown as SEQ ID NO: 10 in the sequence listing of the specification. However this sequence has 2 additional residues at its C-terminal.
enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium cellulovorans CBD cross linker protein (CCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as SEQ ID NO: 6 in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                    / Match 36.5%; Score 487; DB 22; Local Similarity 46.8%; Pred. No. 3.1e-39; nes 116; Conservative 12; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by CCATAGGAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nussinovitch A, Shoseyov O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE05747 standard, Protein; 341 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0164140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wet strength; durability;
CBD cross linker protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 340..341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACPQPD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTA-PGPD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 341
                                                                                                                                                                                                                                                                                                         328 AA;
```

and

Shpiegl I;

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binds crystalline with a Kd ranging from 1.5 microM - 0.5 microM, binds crystalline with a Kd ranging from 1.5 microM - 0.5 microM, pref. with a Kd cf.1.2 microM, esp. <1.0 microM. The protein and the encoding DNA are claimed, as is a CBD fusion protein (FP) comprising the CBD and a second protein. The second protein is pref. Protein A, heparinase, a hormone or an enzyme capable of degrading an environmental pollutant, or an HSP, HSP antibody, cross-reactive HSP-related protein or an antigenic portion of this. The CBD and FP may be used in drug delivery, affinity sepus. and diagnostic techniques. CBD nucleic acid may be obtd. from a variety of cell sources that produce CBDs that bind with high affinity and in a reversible manner or that produce CBD encoding mRNA. The preferred (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                        Isolated cellulose binding domain and fusion proteins - with applications. including drug delivery, affinity separations.
                                                                                                                                                                                                                                                                          Shoseyov 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 125pp; English.
                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
(YISS ) YISSUM RES & DEV CO.
                                                                                                             94WO-US04132
                                                                                                                                                          93US-0048164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 51.7
Matches 106; Conservative
                                                                                                                                                                                                                                                                        Goldstein MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic techniques
                                                                                                                                                                                                                                                                                                                   WPI; 1994-341767/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 AA;
                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ72917
                     WO9424158-A1
                                                                                                           14-APR-1994;
                                                                                                                                                          14-APR-1993;
                                                                27-0CT-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE05745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                        Doi RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE05745
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.
The method involves treating the polysaccharide structure with a
polysaccharide binding domain (BBD) fusion protein. The method is
used to alter the structural, chemical, physical, electrical and
mechanical properties of polysaccharide materials such as paper,
yarns, fibers and textiles, using biological crosslinking agents.
The polysaccharide containing materials have improved mechanical
properties anch as wet strengths, durability and elasticity. The PBD
reagent is applied in the forming stage in fluting paper manufacture
which eliminates the sizing step. The use of a biological crosslinker
if improves the recyclability of paper products. The PBD reagent maintains
the fiber in a slurry therefore resulting in better recovery of
raw materials. The PBD molecules are eluted by strong alkaline conditions
which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strong alkaline conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 -----GRITKSDWSNYTQTNDYSFDASSSTPVVNP-------KVTGYIGGAK--VL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLANDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                   Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------KKGQFITIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is Clostridium cellulovorans cellulose binding domain (CBD) cross linker protein (CCP).

Note: This sequence is stated to be the same as that shown as SEQ ID NO: 6 in the sequence listing of the specification. However this sequence has an additional residue at its C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
36.5%; Score 487; DB 22;
Best Local Similarity 46.8%; Pred. No. 3.3e-39;
Matches 116; Conservative 12; Mismatches 30;
                                                                                                                                                                           Example 1.2; Fig 2b-2e; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR63634 standard; Protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cellulose binding domain; CBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium cellulovorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellulose binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTA-PGPD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 GTACPOPD 246
                   2001-457121/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 AA;
                WPI; 2001-457121/
N-PSDB; AAD11044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        penetrate paper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR63634;
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LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                   121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property;
                                                                                                                      1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                           MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                 Gaps
                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium cellulovorans cellulose binding domain (CBDclos).
                                                                                                                                                                                                                                                                                                                                                                                                                              -----KKGOFITIO
      Length 162;
                                                              14; Indels
                                                                                                                                                                                                                                                                                  36.2%; Score 483; DB 15;
51.7%; Pred. No. 2.8e-39;
tive 9; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                              ------FGFASGRATL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GRITKSDWSNYTQTNDYSFD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE05745 standard; Protein; 163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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SXXXXXXXXXXXXXX

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Clostridium cellulovorans protein A-cellulose binding domain.
                                       24-SEP-2001
                AAE05748;
    linking and/or modifying the properties of polysaccharide materials. The method involves treating the polysaccharide structure with a polysaccharide binding domain (PBD) Gusion protein. The method is used to alter the structural, chemical, physical, electrical and mechanical properties of polysaccharide materials such as paper, yarns, fibers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker improves the recyclability of paper products. The PBD reagent maintains the fine fibers in a slurry therefore resoluting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                        Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Clostridium cellulovorans cellulose binding domain, wet strength; durability; elasticity; CBDclos; cellulose binding protein A; CBP A.
                                                                                                                                                                                                                                                                                                                                                                      present invention relates to methods and compositions for cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is Clostridium cellulovorans cellulose binding domain (CBDclos) of cellulose binding protein A (CBP A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.2%; Score 483; DB 22; Length 163; ilarity 51.7%; Pred. No. 2.8e-39; Conservative 9; Mismatches 14; Indels 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KKGQFITIQ-
                                                                                                                                                                                              YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                            Example 1.1; Page 111-112; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GRITKSDWSNYTQTNDYSFD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                                          Shoseyov O;
                                                                                                                                                                                  (CBDT-) CBD TECHNOLOGIES LTD
                                                                                                                                             99US-0164140.
99US-0166389.
                                                                                                                     02-NOV-2000; 2000WO-IL00708
                                       Clostridium cellulovorans.
                                                                                                                                                                                                                        Nussinovitch A,
                                                                                                                                                                                                                                                 WPI; 2001-457121/49.
N-PSDB; AAD11042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     penetrate paper.
                                                                WO200134091-A2
                                                                                                                                               08-NOV-1999;
                                                                                                                                                          18-NOV-1999;
                                                                                         17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                                                                    property
                                                                                                                                                                                                                        Levy I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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RESULT 13 AAE05748 ID AAE05748 standard; Protein; 428 AA.

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The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.

The method involves treating the polysaccharide structure with a
polysaccharide binding domain (PBD) fusion protein. The method is
used to alter the structural, chemical, physical, electrical and
mechanical properties of polysaccharide materials such as paper,
yarns, fibers and textiles, using biological crosslinking agents.
The polysaccharide containing materials have improved mechanical
properties such as wet strengths, durability and elasticity. The PBD
reagent is applied in the forming stage in flutting paper manufacture
which eliminates the sizing step. The use of a biological crosslinker
improves the recyclability of paper products. The PBD reagent maintains
the fine fibers in a slurry therefore resulting in better recovery of
raw materials. The PBD molecules are eluted by strong alkaline conditions
which enhances the ability of the alkaline glue used in binding to
Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; protein A-cellulose binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Encoded by TAG"
427..428
/note= "These residues are absent in the sequence shown as SEQ ID NO: 8 in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is Clostridium cellulovorans Protein A-cellulose binding domain (ProtA-CBD). This sequence contains a part of CBP A protein and a part of protein A derived from pRIT2T vector sequence. Note: This sequence is stated to be the same as that shown as SEQ ID No: 8 in the sequence listing of the specification. However this sequence has 2 additional residues at its C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of a polysaccharide containing material having at least desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                    1..263
/label= Protein A
/note= "This region is derived from pRIT2T vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1.3; Fig 3b-3g; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       265..426
/label= CBP_A_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shoseyov 0;
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Unknown
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                                                                                                                                                                                                         Clostridium cellulovorans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-457121/49.
N-PSDB; AAD11045.
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                                                                                                                                                        Sequence
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                                                                                                             270 MSVEFYNSNKSAQINSITPIIKIINISDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 329
                                                                                                                                                                                     361
                                                                                                                                                     LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                              121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                               ------KKGQFITIQ------ 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Luciferase; green fluorescent protein; GFP; screening assay; diagnosis; bloluminescence-generating system; toy; cosmetic; fairy dust; beverage; body paint; squirt gun; balloon; slimy play material; soap; toothpaste; fusion protein.
                                                                                          1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Renilla mulleri, Gaussia and Pleuromamma luciferase and
Renilla and Ptilosarcus green fluorescent protein nucleic acids -
                                                                                                                                                                      330 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE----------
                                                             16;
                                 Length 428;
                                                             14; Indels
                               Score 483; DB 22;
Pred. No. 1.1e-38;
                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaussia luciferase fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 222-223; 233pp; English.
                                                                                                                                                                                                                                   | | | | | :
                                                                                                                                                                                                                                                                          181 EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                                                                                                                       ----GRITKSDWSNYTOTNDYSFD 400
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98US-0089367.
98US-0102939.
                               36.2%;
51.7%;
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                                                            106; Conservative
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N-PSDB; AAZ27550.
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                           Query Match
Best Local Similarity
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15-JUN-1998;
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SQ · Sequence
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                                                            Matches
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61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVEFGFASGAATLKKGQFITIQGRITKSDWS 120
balloons, personal items, dentrifrices, soaps, body paints, bubble bath, ink or paper products. In particular, they can be used in e.g. squirt guns, pellet guns, finger paints, foot bags, greeting cards, slimy play material, clothing, bubble making toys, bath powders, cosmetics, body lotions, gels, body paints, bubble bath, inks, wrapping paper, gelatins, icings, frostings, greeting cards, beer, wine, champagne, soft drinks, icings, frostings, greeting cards, beer, wine, champagne, soft drinks, ice cubes, ice, dry ice or fountains. The nucleic acids can also be used to produce transgenic fish and plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCL---QGSSLIIISVFLVGCAQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Green fluorescent protein; GFP; bioluminescence generating system; toy; luciferase; finger paint; slimy play material; fishing lure; sparkler; doll; balloon; personal care item; cosmetic; bath powder; body cream; tooth paste; mouth wash; soap; body paint; ornamental transgenic plant; bubble bath; fountain; fairy dust; food; gelatin; icing; frosting; beer; wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage; dry ice; textile; clothing; paper product; greeting card; wrapping paper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGTFWCDHAGAL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding Renilla reniformis green fluorescent proteins, useful in diagnostic bioluminescence procedures -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 62.69
Matches 107; Conservative
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(BRYA/) BRYAN B J.
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N-PSDB; AAD22201.
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also relates to sequences of the bioluminescence generating system (e.g. luciferase). R. reniformis GFP are used in diagnostic methods and in the production of novelty items such as toys (e.g. squirt gun, pellet gun, toy "Halloween" eggs, toy cigarettes, board/card game toys), finger paints, slimy play material, bubbles in bubble making toys, fishing lures, dolls, sparklers, magic wand toys, balloons, personal care item (e.g. cosmetic, bath powders, body remans, tooth pastes, mouth wash, soaps, body paints, bubble bath), ornamental transgenic plants, fountain, fairy dust, food (gelatins, icings, transgenic plants, champagne, milk, soft drinks, ice cubes, ice, dry ice, beverage), textile (foot bag, clothing) and/or paper product (greeting cards, wrapping paper). The present sequence is CBD-luciferase fusion protein from Gaussia species.
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Sequence 382 AA;

61 LGNSYVDNTSKVTANFVKETASPISTYDTYVEFGFASGAATLKKGQPITIQGRITKSDWS 120 61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCL---QGSSLIIISVFLVGCAQ 117 1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60 1 MSVEFYNSNKSAQTNSITPIIKIINTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60 Query Match 36.0%; Score 480.5; DB 23; Length 382; Best Local Similarity 62.6%; Pred. No. 1.7e-38; Matches 107; Conservative 10; Mismatches 33; Indels 21; Gaps 118 NFSRQ-----EVGAATGAVVGGVAGQLFGKGSGRVSMAIGGA-VLGGLIGS 162 g ઠે 엄 ò

Search completed: November 5, 2003, 20:12:51 Job time: 47.4249 secs

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Sequence 1, Appli
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Sequence 2, Appli
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Sequence 22, Appl
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                                                                                                                                 2003, 20:11:02 ; Search time 16.3592 Seconds (without alignments) 662.108 Million cell updates/sec
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1335
1 MSVEFYNSNKSAQTNSITPI......IYGTACPQPDGRWQVISTEK 256
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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5.1.6
Compugen Ltd.
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US-09-252-991A-23334
US-07-862-588B-2
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US-08-048-164A-2
US-08-460-457-2
US-08-460-457-2
US-08-460-458-2
US-08-460-458-2
US-08-030-394A-2
US-09-006-656-7
US-09-325-274-7
US-09-330-394A-29
US-08-330-394A-29
US-08-330-394A-29
US-08-330-394A-29
US-08-330-394A-29
US-09-339-159B-4
US-09-139-159B-4
US-09-139-159B-4
US-09-139-159B-4
US-09-139-159B-4
US-09-130-136-11-10
US-09-670-11-10
US-09-670-11-10
US-09-136-574A-47
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GenCore version (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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1751
192
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                                                                                                                                                                                                                            Title:
Perfect score:
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                                                                                           protein
                                                                                                                                                                                                                                                                            Sequence:
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                                                                                                                                   Run on
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Sequence 22, Application US/09277716A

Sequence 22, Application US/09277716A

Sequence 22, Application US/09277716A

Sequence 22, Application US/09277716A

GENERAL INFORMATION:
APPLICANT: Bryan, Bruce

APPLICANT: BROLUME, LUTD

TITLE OF INVENTION: LUTPERASES, FLUORESCENT PROTEINS, NUCLBIC ACIDS ENCODING THE
CURRENT APPLICATION NUMBER: US/09/277,716A

CURRENT APPLICATION NUMBER: 06/102,939

EARLIER APPLICATION NUMBER: 60/089,367

EARLIER PELING DATE: 1998-10-01

EARLIER PELING DATE: 1998-6-15

EARLIER PELING DATE: 1998-03-27

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PATENTY OF SEQ ID NOS: 32

LENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Cellulose Binding Domain (CBD)-Gaussia luciferase fusion protein
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                                   115, Appl
11960, Ap
70680, Ap
76628, Ap
26658, Ap
8009, Ap
42816, Ap
28397, Ap
4442, Appli
4253, Ap
       Appl
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12, Appl
12, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVBFGFASGAATLKKGQFITIQGRITKSDWS
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                                                                                           Sequence
Seq
                            Sequence
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Sequence
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       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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US-09-252-991A-21754
US-09-198-452A-15
US-09-198-452A-15
US-09-328-352-7068
US-09-328-352-7068
US-09-328-352-7802
US-09-328-352-8009
US-09-328-352-8009
US-09-328-352-4423
US-09-328-352-4442
US-09-328-352-4442
US-10-092-246-2
US-09-314-001C-4469
US-09-314-001C-4469
US-09-314-001C-4469
US-09-314-001C-4469
US-08-440-519-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |::: ::| | | | 121 NYTQTNDYSFDASSSTPVVNPKVTGY-
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US-09-600-161B-22
; Sequence 22, Application US/09609161B
; Patent No. 6436682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 107; Conservative
    Best Local Similarity
    RESULT 1
US-09-277-716-22
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    Query Match
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GENERAL INFORMATION:

APPLICANT: Shoseyov, Oded
APPLICANT: Shoisel, Itai
APPLICANT: Shoisel, Itai
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: METHODS OF USE OF CELLULOSE BINDING DOMAIN PROTEINS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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Pred. No. 3.8e-41;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,462
FILING DATE: concurrently herewith
CLASSIFICATION: 435
FILON APPLICATION DATA:
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAMB: Misrock, S. Leblie
REGISTRENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7809-006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LGNSYVDNTSKVTANFVKETASPISTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS_DOS
  REFERENCE/DOCKET NUMBER: 7809-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-460-462-2; Sequence 2, Application US/08460462; Patent No. 5670623
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                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                             TYPE: amino acids
TOPOLOGY: lim
                                                                                                                                                                                                                                                                                                                                  Query Match 35.7%;
Best Local Similarity 97.8%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 162 amino acids
amino acid
SY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                             TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-048-164A-2
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LID.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUCTITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIG TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-121B
FILE REFERENCE: 24729-121B
FUNENTY APPLICATION NUMBER: US/09/609.161B
CURRENT FILING DATE: 12995-03-26
PRIOR APPLICATION NUMBER: 09/277,716
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR FILING DATE: 1998-10-01
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Cellulose Binding Domain (CBD)-Gaussia luciferase fusion protein
US-09-609-161B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVBFGFASGAATLKKGQFITIQGRITKSDWS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHWRGCL---QGSSLIIISVFLVGCAQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSVEFYNSNKSAQTNSITPIIKITNTSBSBLNLNDVKVRYYYTSBGTQGQTFWCDHAGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 NFSRQ-----EVGAATGAVVGGVAGQLFGKGSGRVSMAIGGA-VLGGLIGS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----IGGAKVLGTAPGS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Goldstein, Marc A.
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: CELLULOSE BINDING DOWAIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/048,164A
FILING DATE: 14-APR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
36.0%; Score 480.5; DB 4;
Best Local Similarity 62.6%; Pred. No. 5.8e-41;
Matches 107; Conservative 10; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence: fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08048164A Patent No. 5496934 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 18,872
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NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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Sequence 2, Application US/08460458
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                                                1 MSVEFYNSNKSAQTNSITFIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                   6 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
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                    0; Gaps
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                                                                                                                                                                                                                        Sequence 2, Application US/08460457
Patent No. 5719044
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Goldstein, Marc A.
APPLICANT: Goldstein, Marc A.
TITLE OF INVENTIONS: 21
CORRESPONDENCE: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 477; DB 1; Length 162;
Pred. No. 3.8e-41;
2; Mismatches 0; Indels
97.8%; Pred. No. 3.8e-41; trive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                                                  66 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LGNSYVDNTSKVTANFVKETASPISTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7809-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 97.8%;
Matches 90; Conservative 7
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 162 amino acida
TYPE: amino acid
Best Local Similarity 97.8
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-460-457-2
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RESULT 6 US-08-460-458-2

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Patent No. 5738984
GRNERAL INFORMATION:
APPLICANT: Shoseyov, Oded
TITLE OF INVENTION: KITS AND METHODS OF DETECTION USING CELLULOSE BINDING DOMAIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDCTQGQTFWCDHAGAL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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; Sequence 2, Application US/08460455
; Sequence 2, Application US/08460455
; Patent No. 5837814
; GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Sholegil, Ital
APPLICANT: Odidstein, Marc A.
TILLE OF INVENTION: CELLULOSE BINDING DOMAIN PROTEINS
INTHE OF INVENTION: CELLULOSE BINDING DOMAIN PROTEINS
NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,458
FILING DATE: concurrently herewith
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 18,972
REFERENCE/OCCET NUMBER: 18,972
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                                                                                                                                                                          ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELES: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 162 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-458-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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REFERENCE/DOCKET NUMBER: 7809-005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
TITLE OF INVENTION: METHODS OF DETECTION USING THE
TITLE OF INVENTION: CELLULOSE BINDING DOWAIN
NUMBER OF SEQUENCES: 33
CORRESSER: PENNIE & EDWONDS
ADDRESSER: PENNIE & EDWONDS
STREET: NEW YORK
STRATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
CONDITOR: U.S.A.
ZIP: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
APPLICATION NUMBER: US/08/330,394A
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING DATE: 14-APR-1994
ATTORNEY/AGENT: INFORMATION:
ANDAR: NUMBER: LEGITOR
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARES: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,455
FILING DATE: CONCURTENTLY herewith
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US/08/164
FILING DATE: 14-APR-1993
ATYORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REBREENCE/DOCKET NUMBER: 18,872
REBREENCE/DOCKET NUMBER: 18,872
REBREENCE (212) 790-9090
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 66141 PENNIE
SELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 LGNSYVDNTSKVTANFVKETASPISTYDIYVE 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity 97.8<sup>†</sup>
Matches 90; Conservative
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6 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 65
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Patent No. 6005092

GENERAL INFORMATION:
APPLICANT: Shosey, Oded
TITLE OF INVENTION:
TITLE OF INVENTION: GLUCANASE GENE, PROMOTER AND PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 35.7%; Score 477; DB 3; Length 163; Best Local Similarity 97.8%; Pred. No. 3.8e-41; Matches 90; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        35.7%; Score 477; DB 2; Length 162; 97.8%; Pred. No. 3.8e-41; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGNSYVDNTSKVTANFVKETASPISTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,636
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7809-019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7809
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 759-9090
TELEFRAX: (212) 869-8864
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: 110-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATINE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 97.8%
Matches 90, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: peptide US-09-006-636-7
                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-330-394A-2
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STAIR: ...
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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                                                                                                                                                                                                                                           COMPUTER: IBM COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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US-08-330-394A-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
1 MSVEFYNSNKSAQTNSITFIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                       7 MSVEPYNSNKSAQINSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 66
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                                                                                                                                                                                                             Sequence 7, Application US/09006632
Patent No. 618440
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shani, Ziv
APPLICANT: Shani, Ziv
ITILE OF INVENTION: TRANSGENIC PLANTS OF ALTERED
TITLE OF INVENTION: MORPHOLOGY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                     67 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7809-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 1003 6-271

ZIP: 1003 6-271

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FSSTEM: DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/006,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09325274
Patent No. 6323023
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shani, Ziv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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US-09-325-274-7
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TITLE OF INVENTION, CAUCHARS GENE, PROMOTER AND PROTEIN
WUNDERS OF SEQUENCES:
CORRESPONDEME AND PROTEIN
CORPUTER FRANCE PERMIS EMACRACT
CORRESPONDEME AND PROTEIN
CORPUTER FRANCE AND PROTEIN
CORPUTER FRANCE AND PROTEIN
CORPUTER REDAILS FORM:
WEDDIM TYPE: DISACTER
CORPUTER FRANCE AND PROTEIN
COR
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1 SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL. 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yeda Research and Development Co. Ltd.
APPLICANT: Ramot University Authority for Applied
APPLICANT: Research and Industrial Development Ltd.
APPLICANT: Technion Research and Development Edd.
APPLICANT: Bayer, Edward A.
APPLICANT: Wilchek, Meir
APPLICANT: Wilchek, Meir
APPLICANT: Shoham, Yuval
APPLICANT: Shoham, Yuval
APPLICANT: Shoham, Yuval
APPLICANT: Lamed, Raphael
APPLICANT: APPLICANT: APPLICANT: TITLE OF INVENTION: MODIFIED CELLULOSE-BINDING DOWAIN (CBD)
TITLE OF INVENTION: PROTEINS AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                      Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13813
                                                                                                                                                                                                                                                                                                                                                                           Score 472; DB 2;
Pred. No. 1.2e-40;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GNSYVDNTSKVTANFVKETASPTSTYDTYVE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application PC/TUS9513813 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: BAYEI
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 628-5197
TELERAX: 248633
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
| CELEFAX: (2.12) 669-8864 | TELEX: 66441 PENNIE | TELEX: 66441 PENNIE | SEQUENCE CHARACTERISTICS: LENGTH: 156 Amin.
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.8%;
Matches 89; Conservative
                                                                                                                                                                           : 156 amino acids amino acids
                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-330-394A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Browdy an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20004
                                                                                                                                                                                                          TYPE: amir
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                            CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/330,394A
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING DATE: 14-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REFERENCE/DOCKET NUMBER: 7809-005
TELLEFAX: (212) 790-9090
TELLEFAX: (212) 790-9090
TELLEFAX: (212) 790-9090
TELLEFAX: (212) 790-9090
TELLEFAX: (212) 864
TELLEFAX: (A12) 864
TELLEFAX: AMANGER: AMANGER: SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS:
ILENGTH: 154 amino acids
TYPE: amino acid
TYPE: AMANGER: LIBERAY
TO AMANGER AMANGER: AMANGER: AMANGER AMAN
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APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Yosef, Karmey
APPLICANT: Shpiegl, Itai
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: METHODS OF DETECTION USING THE
TITLE OF INVENTION: CELLULOSE BINDING DOMAIN
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.4%; Score 472; DB 2; L 97.8%; Pred. No. 1.1e-40; tive 2; Mismatches 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,394A
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GNSYVDNTSKVTANFVKETASPISTYDIYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GNSYVDNTSKVTANFVKETASPTSTYDTYVE 91
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STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-330-394A-22,
; Sequence 22, Application US/08330394A
; Patent No. 5856201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MISROCK, S. LESLIE
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 97.8°
Matches 89; Conservative
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MEDIUM TYPE:
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                                                                                                       1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
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                                                                                                                                            4; Gaps
                                                         4; Gaps
Query Match 18.4%; Score 245; DB 5; Length 167; Best Local Similarity 51.5%; Pred. No. 2.4e-17; Matches 53; Conservative 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
18.4%; Score 245; DB 4; Length 476;
Best Local Similarity 51.5%; Pred. No. 1.1e-16;
Matches 53; Conservative 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                    68 IGSNGSYNGITSNVKGTFVKMSSS-TNNADTYLEISFTGGTLE 109
                                                                                                                                                                                                                    61 LGN--SYVDNTSKVTANFVKETASPISTYDTYLDPSHMRGCLQ 101
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4 Application US/09339159B

Patent No. 6566114

GENERAL INFORMATION:

APPLICANT: Kauppinen, Markus

APPLICANT: Schulein, Martin

APPLICANT: Andersen, Lene

APPLICANT: Biornvad, Mads

TITLE OF INVENTION: No. 6566114el Mannanases

TITLE OF INVENTION: No. 6566114el Mannanases

CURRENT APPLICATION NUMBER: US/09/339,159B

CURRENT FILING DATE: 1999-06-24

NUMBER OF SEQ ID NOS: 55

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Bacillus
US-09-339-159B-4
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US-09-339-159B-4
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5, 2003, 20:16:47 Search completed: November Job time: 17.3592 secs

318 LKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGQKDQTFWCDHA-AI 376

g 8 g

61 LGN--SYVDNTSKVTANFVKETASPISTYDTYLDPSHMRGCLQ 101

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November 5, 2003, 20:15:12; Search time 30.0656 Seconds (without alignments) 1462.395 Million cell updates/sec
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1335
1 MSVEFYNSNKSAQTNSITPI......IYGTACPQPDGRWQVISTEK 256
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/ cgn2 6/ptodata/2/pubpaa/USO7 PUBCCMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO6 PUBCCMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO8 PUBCCMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO8 PUBCCMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO8 PUBCCMB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*

/ cgn2 6/ptodata/2/pubpaa/USO0 NEW PUB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  644079 seqs, 171749292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                              Copyright
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                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |   |        | Description | Sequence 6, Appli | Sequence 4, Appli | Sequence 2, Appli | Sequence 22, Appl | Sequence 12, Appl | Sequence 29, Appl | Sequence 169, App | Sequence 2, Appli | 8                  | Sequence 4, Appli | Sequence 6, Appli | 9               | Sequence 5, Appli | Sequence 5, Appli | Sequence 1, Appli |
|-----------|---|--------|-------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-----------------|-------------------|-------------------|-------------------|
| SUMMARIES |   |        | αi          | US-10-261-446-6   | US-10-261-446-4   | US-10-261-446-2   | US-09-808-898-22  | US-10-072-152-12  | US-09-955-555A-29 | US-10-127-032-169 | US-09-784-554B-2  | US-10-156-761-8100 | US-09-784-554B-4  | US-09-917-384-6   | US-09-917-383-6 | US-09-917-384-5   | US-09-917-383-5   | US-09-917-384-1   |
|           |   |        | - 1         | 12                | 12                | 12                | 11                | 14                | 11                | 15                | 11                | 15                 | 11                | 11                | 11              | 11                | 11                | 11                |
|           |   | Query  | Length      | 256               | 161               | 162               | 382               | 493               | 599               | 182               | 1352              | 741                | 1350              | 1043              | 1043            | 150               | 150               | 1228              |
|           | ф | Query  | Match       | 100.0             | 62.3              |                   |                   |                   |                   |                   | 9.6               | 9.5                | 9.5               | 9.3               | 9.3             | 9.1               | 9.1               | 9.1               |
|           |   |        | Score       | 1335              | 832               | 815               | 480.5             | 245               | 245               | 127.5             | 127.5             | 127                | 126.5             | 123.5             | 123.5           | 121               | 121               | 121               |
|           |   | Result | No.         | н                 | 7                 | c                 | 4                 | 'n                | 9                 | 7                 | 80                | 6                  | 10                | 11                | 12              | 13                | 14                | 15                |

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Gaps

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100.0%; Score 1335; DB 12; Length 256; 100.0%; Pred. No. 1.4e-128; ive 0; Mismatches 0; Indels 0;

Matches 256; Conservative Query Match Best Local Similarity

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9 9 61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120

1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL

| Sequence 1, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 28, Appl  | IMMUNITY IN FISH A   |
|---|--|
| 1 US-09-917-383-1<br>1 US-09-917-378-4<br>1 US-09-917-378-4<br>5 US-10-155-400-1<br>5 US-10-155-400-4<br>5 US-10-155-400-4<br>5 US-10-185-990-10<br>2 US-10-185-990-10<br>2 US-09-978-295-28<br>0 US-09-978-295-28<br>1 US-09-978-295-28<br>1 US-09-978-1914-28<br>1 US-09-978-1914-28<br>1 US-09-978-1914-28<br>1 US-09-978-1914-28<br>1 US-09-978-1914-28<br>1 US-09-978-1914-28<br>1 US-09-978-1914-28<br>1 US-09-918-584-28<br>1 US-09-918-584-28<br>1 US-09-918-584-28<br>1 US-09-918-1914-28<br>1 US-09-978-1918-28<br>1 US-09-978-1918-28<br>1 US-09-978-1918-28 | ALIGNMENTS 1446  LD AGENTS FOR AL DISEASES, 710/261,446 30 9/677,374 0/154,437 monis   |
| 10000000000000000000000000000000000000  | -6 Application US/102614* No. US20030165526A1 ORWATION: Karyk, Michel A. Burian, Jan Ray, William W. Thornton, Julian C. WYENTION: VACCINES AND NYENTION: RTCKETYSIAL ENDE: 4616-64094 PLICATION NUMBER: US/01 CLING DATE: 2002-09-30 ICATION NUMBER: US 60/1 NG DATE: 1999-09-17 SEQ ID NOS: 20 Patentin version 3.0 56 Piscirickettsia salmon SIGNAL (-95)(-1)   |
| 1120.21<br>120.21<br>120.021<br>1111.11.11.11.11.11.11.11.11.11.11.11.  | ESULT 1 S-10-261-446-6 Sequence 6, Application US/10261 APPLICANT: Burian, Jan APPLICANT: Burian, Jan APPLICANT: Tornton, Juliam W. APPLICANT: Tornton, Juliam W. APPLICANT: Tornton, Juliam W. APPLICANT: Tornton, Juliam W. TITLE OF INVENTION: VACCINES AN TITLE OF INVENTION: VACCINES AN TITLE OF INVENTION: RICKETF314 CURRENT FILING DATE: 2002-09-3 PRIOR PILING DATE: 2000-09-15 PRIOR FILING DATE: 1999-09-17 WUMBER OF SEQ ID NOS: 20 SOFTWARE: PATENTIN VARIEN: US 60 LENGTH: 256 TYPE: PAT ORGANISM: PISCITICKETTSIA SAIM FRATURE: NAME/KEY: SIGNAL LOCATION: (-95)(-1)   |
|   | RESULT 1 US-10-261-446- SEQUENCE 6, PUDLICATON APPLICANT: APPLICAN |

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APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, William
TITLE OF INVENTION: RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING 1
TITLE OF INVENTION: ELOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH TH
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
TITLE OF INVENTION: 2001-03-15
CURRENT APPLICATION NUMBER: 05/03-15
PRIOR FILING DATE: 2000-03-15
PRIOR PELING DATE: 1996-03-26
PRIOR PELING DATE: 1996-12-35
PRIOR APPLICATION NUMBER: 08/757,046
PRIOR APPLICATION NUMBER: 08/757,046
PRIOR APPLICATION NUMBER: 08/957,274
PRIOR APPLICATION NUMBER: 08/957,274
PRIOR APPLICATION NUMBER: 08/99,103
PRIOR APPLICATION NUMBER: 08/990,103
PRIOR APPLICATION NUMBER: 08/990,103
PRIOR APPLICATION NUMBER: 08/990,103
PRIOR APPLICATION NUMBER: 08/990,103
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                                                                                                                                                                                                                                                                                                                                                                                                                                      97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                             Score 815; DB 12; Length 162;
Pred. No. 1.5e-75;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 ROOYCREFQOKAMIAGQKQEIYGTACROPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ 1D NOS: 20
SOFFWARE: Patentin version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                     ) ORGANISM: Piscirickettsia salmonis
US-10-261-446-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 22, Application US/09808898; Publication No. US20030092098A1
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Best Local Similarity 98.8%;
Matches 158; Conservative 1
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Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-808-898-22
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                                                                                                                                                                                                LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217
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                                                                                                                                                                                                                          TYPE: PRT
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APPLICANT: BUTIAN, JAN
APPLICANT: KAY, William W.
APPLICANT: KAY, WILLIAM W.
APPLICANT: KAY, WILLIAM W.
APPLICANT: KAY, WILLIAM W.
APPLICANT: TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: VANDER: US/10/261,446
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VARIETIES
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10261446
Publication No. US20030165526A1
GENERAL INFORMATION:
APPLICANT: KLZYK, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Thornton, Juliam W.
APPLICANT: Thornton, Juliam C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPRENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 LGGLIGSKIGQSMDQODKIXLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
                                                                                                                    121 ROEVGAATGAVVGGVAGOLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
  1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                   181 EKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGT
                                                                                       RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
                                                                                                                                                                                                181 EKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10261446 Publication No. US20030165526A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            241 ACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                  241 ACPÓPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kuzyk, Michael A. APPLICANT: Burian, Jan
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US-10-261-446-2
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Sequence 169, Application US/10127032
Publication No. US20030113742A1
GENERAL INFORMATION:
APPLICANT: Whiteley, Maryin
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                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Clostridium thermocellum
US-09-955-555A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                   18.4%;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.5;
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-127-032-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-127-032-169
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US-09-784-554B-2
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61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVEFGFASGAATLKKGQFITIQGRITKSDWS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                118 NFSRQ-----EVGAATGAVVGGVAGQLFGKGSGRVSMAIGGA-VLGGLIGS 162
                                                                                                  ---IGGAKVLGTAPGS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blornvad. Mad8 E.
APPLICANT: Blornvad. Mad8 E.
APPLICANT: Glad, Sanne O. S.
APPLICANT: Glad, Sanne O. S.
APPLICANT: Gampinen, Markus S.
APPLICANT: Schoncr, Kirk
APPLICANT: Schoncr, Kirk
APPLICANT: Schoncr, Kirk
APPLICANT: Kongsbak, Lars
TITLE OF INVENTION: No. US20020142438Alel Pectate Lyases
TITLE OF INVENTION: No. US20020142438Alel Pectate Lyases
TITLE OF INVENTION: No. US20020142438Alel Pectate Lyases
TITLE OF INVENTION: NUMBER: US/19/19/19/
PRIOR APPLICATION NUMBER: 134/97
PRIOR PILLING DATE: 1997-11-24
PRIOR FILLING DATE: 1997-11-24
PRIOR FILLING DATE: 1997-11-20
PRIOR FILLING DATE: 1997-11-20
PRIOR FILLING DATE: 1997-11-20
PRIOR FILLING DATE: 1998-05-06
PRIOR FILLING DATE: 1998-05-06
PRIOR FILLING DATE: 1998-11-02
PRIOR FILLING DATE: 1998-11-02
PRIOR FILLING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 32
SOFFWARE: PastSEQ for Windows Version 4.0
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Publication No. US20030027298A1
GENERAL INFORMATION:
APPLICANT: Bott, Richard R.
APPLICANT: Fowler, Timothy
APPLICANT: Fowler, Timothy
APPLICANT: Mard, Michael
APPLICANT: Xia, Hall-Ying
APPLICANT: Xia, Hall-Ying
APPLICANT: Xia, Hall-Ying
APPLICANT: Sia, Hall-Ying
APPLICANT: Siame
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                                                                                ORGANISM: Clostridium thermocellum
                                                                                                                                                                                                                           Sequence 12, Application US/10072152
Publication No. US20020142438A1
                                                                                                                                                                                                                                                                                                                                Schulein, Martin
Lange, Niels E.
Bjornvad, Mads E.
                                                                                                                                                                                                                                                                                                           APPLICANT: Andersen, Lene N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-955-555A-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 ÓIAGTAIGAVVGGLLGNQIGGGTGKKIATVAGAVGGGYAGNKVQEGMQERDTYTTTETRC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bangera, M. Gita
APPLICANT: Bangera, M. Gita
APPLICANT: Lory, Stephen
APPLICANT: Greenberg Everett Peter
TITLE OF INVENTION: BIOPILM FORMATION
FILE REPERENCE: UIZ-070CP
CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT APPLICATION NUMBER: US 60/285,190
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR APPLICATION NUMBER: US 60/344,142,
PRIOR APPLICATION NUMBER: US 60/344,142,
PRIOR APPLICATION NUMBER: US 60/344,142,
PRIOR FILING DATE: 2001-04-20,
NUMBER OF SEQ ID NOS: 170
SOFTWARE FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LGN--SYVDNTSKYTANFVKETASPTSTYDTYLDPSHMRGCLQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 245; DB 11;
Pred. No. 2.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 -KLNOSLEKV------KAGOVTRWRNP 194
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FILE REPERENCE: GC278-C3
CURRENT APPLICATION NUMBER: US/09/955,555A
CURRENT APPLICATION NUMBER: US/09/959,958
PRIOR APPLICATION NUMBER: US 60/005,701
PRIOR FILING DATE: 1995-11-17
PRIOR FILING DATE: 1995-10-17
NUMBER OF SEQ ID NOS: 29
SOFWMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
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Gaps

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1202 LQYRTADINVNDNHLNPHPQILNKGTISVPINELKIRYYYTIDGDREQTFNCDYA---- 1256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALLG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFW-CDHAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----STDNVGVAHYNVYRNGVLVGQPTVTSFTDTG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6. Application US/09917384
; Publication No. US20030096342A1
; Publication No. US20030096342A1
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU
; APPLICANT: VINZANT, TODD B.
APPLICANT: VINZANT, TODD B.
APPLICANT: HIMMEL, MICHAEL B.
; APPLICANT: HIMMEL, MICHAEL B.
; TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
; TITLE OF INVENTION: THERMAL TOLERANT
; FILE REFERENCE: 40170.6US01
; CURRENT APPLICATION NUMBER: US/09/917,384
; CURRENT FILING DATE: 2001-07-28
; NUMBER OF SEQ ID NOS: 14
; SSOTHARE: PATENTIN VET. 2.1
; SEQ ID NO 6
; LENGTH: 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.3%; Score 123.5; DB 11; Length 1043; Best Local Similarity 24.6%; Pred. No. 0.0019; Matches 58; Conservative 28; Mismatches 79; Indels 71;
                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 1350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 LLGNSYVDNTSKVTANFVKETASP-TSTYDTYLDPSHMRGCLQ--GSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Segment OTHER INFORMATION: GUXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1257 ---VLSCSKLNGKLVKMDKAAŤGA-DYYLEVS 1284
                                                                                                                                                                                                                                                                                                                                                                    9.5%; Score 126.5; DB 31.5%; Pred. No. 0.0013; tive 19; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 NSYVDNTSKVTANFVKETASPTSTYDTYLDPS 94
                     APPLICANT: Schulein, Martin
TITLE OF INVENTION: FAMILY 44 XYLOGLUCANASES
FILE REFERENCE: 10017.200-US
CURRENT APPLICATION UNMBER: US/09/784,554B
CURRENT FILING DATE: 2011-02-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PALENTIN version 3.1
                                                                                                                                                                                                                                                                                     ORGANISM: Paenibacillus polymyxa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SSVŠLAWNA---
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                                       LENGTH: 1350
                                                                                                                                                                                                                                                                                                                   US-09-784-554B-4
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                                                                                                                                                                                                            SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105
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                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALLG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSD-GTQGQTFWCDHAGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        9; Gaps
                                                                                                                                                                                                                                                                                                                                                              Query Match
9.6%; Score 127.5; DB 11; Length 1352;
Best Local Similarity 30.4%; Pred. No. 0.001;
Matches 28; Conservative 19; Mismatches 36; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 LLGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCL 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1260 ----SCSKLNGKLVKMEKAATGA-DYYLEVS 1285
                   APPLICANT: Schulein, Martin
TITLE OF INVENTION: FAMILY 44 XYLOGLUCANASES
FILE REFERENCE: 10017.200-US
CURRENT APPLICATION NUMBER: US/09/784,554B
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 NSYVDNTSKVTANFVKETASPTSTYDTYLDPS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: IKEDA, HARUO

APPLICANT: IKEDA, HARUO

APPLICANT: SHIBA, HINOSHI

APPLICANT: SHIBA, HINOSHI

APPLICANT: SHIBA, HINOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: HATTORI, MASAHRRA

TITLE OF INVENTION: NUWBER: US/10/156,761

CURRENT APPLICATION NUWBER: US/2001-20089

PRIOR APPLICATION NUWBER: JP 2001-204089

PRIOR APPLICATION NUWBER: JP 2001-272697

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-06-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8100, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09784554B
, Publication No. US20030032162A1
, GENERAL INFORMATION:
, APPLICANT: Schnorr, Kirk
                                                                                                                                                                                                                                                                                        ORGANISM: Paenibacillus polymyxa
  Jorgensen, Per Lina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-156-761-8100
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APPLICANT:
                                                                                                                                                                                                                                                               TYPE: PRT
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 LLGNSYVDNTSKVTANFVKETASP-TSTYDTYLDPSHMRGCLQ--GSS------ 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 KGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645 ---SSVSLAWNA-----STDNVGVAHYNVYRNGVLVGQPTVTSFTDTG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
9.3%; Score 123.5; DB 11; Length 1043;
Best Local Similarity 24.6%; Pred. No. 0.0019;
Matches 58; Conservative 28; Mismatches 79; Indels 71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-917-384-5

Sequence 5, Application US/09917384

Publication No. US20030096342A1

GENERAL INFORMATION:
APPLICANT: DING, SHI-YOU
APPLICANT: VINZANT, TODD B.
APPLICANT: VINZANT, TODD B.
APPLICANT: WINZANT TODD B.
APPLICANT: WINSANT THEMBL F.
APPLICANT: HIWMEL, MICHAEL E.
TITLE OF INVENTION: CELLULOLYTICUS
FILE REFERENCE: 40170.6US01
CURRENT APPLICATION NUMBER: US/09/917,384

CURRENT FILING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE:
JOTHER INFORMATION: Description of Artificial Sequence: Segment of CHER INFORMATION: GUXA
JG-09-917-384-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence: Segment of CTHER INFORMATION: GuxA US-09-917-383-6
                                                                                   APPLICANT: AND WILLIAM S.
APPLICANT: MINZANT, TODD B.
APPLICANT: DECKER, STEPHER R.
APPLICANT: HUMEL, MICHAEL B.
TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS FILLS OF INVENTION: CELLULCLYTICUS FILLS REFERENCE: 40170 .6USOU CURRENT APPLICATION NUMBER: US/09/917,383
CURRENT FILLING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATCHIN VEY: 2.1
SEQ ID NO 6
Sequence 6, Application US/09917383
Publication No. US20030104522A1
GENERAL INFORMATION:
APPLICANT: DING, SHI-YOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1043
TYPE: PRT
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LENGTH: 150
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1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFW-CDHAGA 59
                                                                                                                                                           1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFW-CDHAGA 59
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APPLICANT: DINO, WILLIAM S.

APPLICANT: DINOY, WILLIAM S.

APPLICANT: ADNEY, WILLIAM S.

APPLICANT: DECKER, STEPHEN R.

APPLICANT: DECKER, STEPHEN R.

TITLE OF INVENTION: THERNAL TOLERANT CELLULASE FROM ACIDOTHERMUS

TITLE OF INVENTION: THERNAL TOLERANT CELLULASE FROM ACIDOTHERMUS

TITLE OF INVENTION: CELLULOLYTICUS

FILE REPERENCE: 40170-6191

CURRENT PILING DATE: 2001-07-28

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PALENTIN VEY: 2.1

SEQ ID NO 5

LENGTH: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Segment of
OTHER INFORMATION: GuxA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.1%; Score 121; DB 11; Length 150; Best Local Similarity 32.4%; Pred. No. 0.00021; Matches 33; Conservative 19; Mismatches 38; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DING, SHI-YOU
APPLICANT: DING, SHI-YOU
APPLICANT: ADNEY, WILLIAM S.
APPLICANT: VIASANT, TODD B.
APPLICANT: VIASANT, TODE B.
APPLICANT: HIMMEL, MICHAEL E.
APPLICANT: HIMMEL, MICHAEL E.
TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
TITLE OF INVENTION: CELLULOLYTICUS
FILE REPERENCE: 40170.60501
CURRENT APPLICATION NUMBER: US/09/917,384
CURRENT APPLICATION NUMBER: 105/09/917,384
SURRENT APPLICATION NUMBER: 14
SURRENT APPLICATION NUMBER: 14
                                                           12;
   Length 150;
                                                           Indels
                                                                                                                                                                                                                                         60 LLGNSYVDNTSKVTANFVKETASP-TSTYDTYLDPSHMRGCL 100
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                                                                                                                                                                                                                                                                           65 GCGN-----IRASF--GSVNPATPTADTYLQLSFTGGTL 96
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9.1%; Score 121; DB 11;
32.4%; Pred. No. 0.00021;
live 19; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 5, Application US/09917383
; Publication No. US20030104522A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09917384
Publication No. US20030096342A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 32.4*
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
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PREATURE:

COTHER INFORMATION: Description of Artificial Sequence: Segment of

COTHER INFORMATION: GuxA

US-09-917-384-1

Query Match

Best Local Similarity 32.4%; Pred. No. 0.0042;

Matches 33; Conservative 19; Mismatches 38; Indels 12; Gaps 4;

Qy 1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFW-CDHAGA 59

CONSERVATIONSAPGDNQIKPGLQLVNTGSSSVDLSTVTVRYWFTRDGGSSTLVYNCDMAAM 647

Qy 60 LLGNSYVDNTSKVTANFVKETASP-TSTYDTYLDPSHWRGCL 100

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5, 2003, 20:10:11; Search time 18.1278 Seconds (without alignments) 1358.089 Million cell updates/sec November Run on:

Title: Perfect score: Sequence:

US-09-677-374-6 1335 1 MSVEFYNSNKSAQTNSITPI......IYGTACPQPDGRWQVISTEK 256

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|               |       | d              |        |    | SUMMAKIES |                    |
|---------------|-------|----------------|--------|----|-----------|--------------------|
| Result<br>No. | Score | Query<br>Match | Length | DB | ID        | Description        |
| -             | 487   | 36.5           | 1848   | 2  | A44140    | cellulose-binding  |
| 7             | 288   | 21.6           | 159    | 7  | D33971    | rickettsial common |
| ٣             | 285   | 21.3           | 159    | ~  | B33971    | Rickettsial common |
| 4             | 285   | н              | 159    | ~  | A33971    | Rickettsial common |
| Ŋ             | 285   | 21.3           | 159    | ~  | G97860    | 17K surface antige |
| 9             | 276.5 | 20.7           | 159    | ~  | C33971    |                    |
| 7             | 276   | 20.7           | 159    | 7  | A25972    | 17K antigen precur |
| æ             | 249   | 18.7           | 586    | 7  | PC6006    |                    |
| σ             | 245   | 18.4           | 1854   | ~  | 836859    |                    |
| 10            | 233.5 | 17.5           | 1162   | 7  | T30433    | scaffolding protei |
| 11            | 223.5 | 16.7           | 1483   | 7  | C97012    | probably celluloso |
| 12            | 188.5 | 14.1           | 879    | 7  | A47704    | endoglucanase I (E |
| 13            | 188   | 14.1           | 986    | ~  | S12021    | 금                  |
| 14            | 151.5 | 11.3           | 1779   | ~  | T31085    | xylanase - Caldice |
| 15            | 147   | 11.0           | 915    | 7  | A43802    |                    |
| 16            | 143.5 | 10.7           | 1039   | ~  | 802711    | cellulase (EC 3.2. |
| 17            | 143.5 | 10.7           | 1331   | ~  | A48954    | mannan endo-1,4-be |
| 18            | 142   | 10.6           | 1711   | ~  | T31337    | 1,4-beta-glucanase |
| 19            | 138.5 | 10.4           | 1742   | 7  | T17120    | cellulase (EC 3.2. |
| 20            | 127.5 | 9.6            | 182    | 7  | D83169    | conserved hypothet |
| 21            | 122   | 9.1            | 257    | ~  | P87413    | hypothetical prote |
| 22            | 121   | 9.1            | 20     | ~  | 669593    | cellulase (EC 3.2. |
| 23            | 120.5 |                | 7      | ~  | AI3418    | 17K surface antige |
| 24            | 115   | 8.6            | 499    | ~  | JN0111    | cellulase (EC 3.2. |
| 25            | 113.5 | 8.5            | 499    | ~  | A27198    | cellulase (EC 3.2. |
| 56            | 112.5 | 8.4            | 155    | ~  | S23787    | outer membrane lip |
| 27            | 111.5 | 8.4            | 154    | ~  | B83514    |                    |
| 28            | 111   | 8.3            | 145    | ~  | A41897    | cellulase homolog  |
| 29            | 109.5 | 8.2            | 508    | 0  | A26874    | cellulase (EC 3.2. |

| outer membrane lip | probable secreted | hypothetical prote | conserved hypothet | lipA protein [impo | probable lipoprote | lipA protein (impo | bifunctional cellu | outer membrane lip | outer membrane lip | probable outer mem | probable outer mem | lipA protein - Rhi | outer membrane pro | cellulase (EC 3.2. | PAL cross-reacting |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AI0693             | AE0644            | G87629             | B82837             | AD2696             | AF0289             | D97478             | I40548             | AG0443             | C64921             | F90922             | B85771             | S58234             | AD3350             | S54744             | 164130             |
| 0                  | ~                 | 7                  | ~                  | 0                  | ~                  | ~                  | ~                  | ~                  | ~                  | 7                  | ~                  | ~                  | ~                  | ~                  | 7                  |
| 155                | 179               | 232                | 257                | 142                | 155                | 125                | 486                | 155                | 155                | 155                | 155                | 139                | 232                | 504                | 155                |
| 8.2                | 8.2               | 8.2                | 8.2                | 8.1                | 8.1                | 8.0                | 8.0                | 8.0                | 7.8                | 7.8                | 7.8                | 7.8                | 7.7                | 7.7                | 7.6                |
| 601                | 109               | 109                | 109                | 107.5              | 107.5              | 107                | 107                | 106.5              | 104.5              | 104.5              | 104.5              | 104                | 103                | 103                | 101.5              |
| -                  |                   |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |

## ALIGNMENTS

RESULT 1

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Cigocosion: A44140
Rishoseyov, O.; Takaqi, M.; Goldstein, M.A.; Doi, R.H.
Proc. Natl. Acad. Scl. U.S.A. 89, 3483-3487, 1992.
A;Title: Primary sequence analysis of Clostridium cellulovorans cellulose binding protest A;Reference number: A44140, MUID:92228810; PMID:1565642
A;Accession: A44440
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-1848 cSHO>
A;Cross-references: GB:M73817; NID:g144748; PIDN:AAA23218.1; PID:g144749
C;Genetics:
cellulose-binding protein A precursor - Clostridium cellulovorans
C;Species: Clostridium cellulovorans
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :06
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 36.5%; Score 487; DB 2; Length 1848; Best Local Similarity 46.8%; Pred. No. 6.7e-32; Matches 116; Conservative 12; Mismatches 30; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: cbpA
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7 9

|   |     |  | 186 | g  |
|---|-----|--|-----|----|
|   |     | 239 GTACPQPD 246   | 239 | ò  |
| _ | 185 |  | 144 | qq |
| _ | 238 | 181 EKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238   | 181 | δ  |
|   | 143 |  | 125 | Dp |
| _ | 180 | 121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180 | 121 | ò  |
|   | 124 | 93 LGNSYYDNISKVIANFVKETASPISTYDTYVE                                  | 93  | Dp |
| _ | 120 | 61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120  | 61  | ò  |
|   | 95  | 33 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 92   | 33  | g  |

### RESULT D33971

rickettsial common antigen precursor - Rickettsia prowazekii
N;Alternate names: 17kD surface antigen; outer membrane protein (omp); RP833
C;Species: Rickettsia prowazekii
C;Date: 16-Mar-1990 #sequence\_revision 16-Mar-1990 #text\_change 03-Nov-2000
C;Accession: D33971; B71645
R;Anderson, B.E.; Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989

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C;Species: Rickettsia rīckettsii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C;Anderson, B.B.; Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Accession: A33971, MUD:89359171; PMID:2768201
A;Accession: A33971
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R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093, 2009, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-159 KURx>
A, Cross-references: GB: ABC006914; PIDN: AAL03825.1; PID: g15620425; GSPDB: GN00173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ::| :|| || :|| :|| 64 GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
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C,Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residuss: 1-159 <AND:
A;Crosa-references: BB:M28480; NID:9152457; PIDN:AAA26376.1; PID:9152458
C;Superfamily: rickettsial common antigen
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21.3%; Score 285; DB 2; Length 159,
Best Local Similarity 37.9%; Pred. No. 1.9e-16;
Matches 61; Conservative 31; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Indels
                                                                                                            Rickettsial common antigen precursor - Rickettsia rickettsii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 KOERROQYCREFQOKAMIAGOKOEIYGTACPOPDGRWQVIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.3%; Score 285; DB 2; ilarity 37.9%; Pred. No. 1.9e-16; Conservative 31; Mismatches 53;
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Best Local Similarity
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A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A33971; MUID:89359171; PMID:2768201
A;Status: D33971
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <AND>
A;Cross references: GB:M28482; NID:g152461
A;Note: the sequence in GenBank entry RIRAWTITKC, release 109.0, (PID:g152462) omits the A;Note: the sequence in GenBank entry RIRAWTITKC, release 109.0, (PID:g152462) omits the R;Andersson, S:G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U Nature: 396, 133-140, 1998
A;Andersson, S:G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature: 396, 133-140, 1998
A;Andersson, S:G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Retus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-159 <AN2>
A;Roseidues: 1-159 <AN2>
A;Roseidues: 1-159 <AN2>
A;Roseidues: 1-159 <AN3>
A;Genetics:

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Cipate: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
Cipatesion: B3371
Riaderson, B.E.; Tzianabos, T.
B. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A33971, MUID:89359171; PMID:2768201
A;Accession: B33971
A;Accession: B33971
A;Accession: B34974
A;Molecule type: DNA
A;Residues: 1-159. <AND.
A;Coss-references: GB:M28479; NID:9152463; PIDN:AAA26379.1; PID:9152464
C;Superfamily: rickettsial common antigen
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C;Species: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
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21.6%; Score 288; DB 2; Length 159;
Best Local Similarity 37.9%; Pred. No. 1e-16;
Matches 61; Conservative 32; Mismatches 52; Indels
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Best Local Similarity
Matches 61; Conserv
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A;Residues: 1-1615,1617-1854 <GE2>
A;Cross-references: EMBL:L08665
R;Fujino, T.; Beguin, P.; Aubert, J.P.
FEMS Microbiol. Lett. 94, 165-170, 1992
A;Title: Cloning of a Clostridium thermocellum DNA fragment encoding polypeptides that }
A;Reference number: $25767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1654 <GER>
A;Cross-references: EMBL:L08665
A;Cross-references: EMBL:L08665
B;Gerngross, U.T.; Romaniec, M.P.M.; Kobayashi, T.; Huskisson, N.S.; Demain, A.L.
Mol. Microbiol. 8, 325-334, 1993
A;Title: Sequencing of a Clostridium thermocellum gene (cipA) encoding the cellulosomal
A;Reference number: S33527; MUID:93302508; PMID:8316083
     the scaffolding protein CipC of
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A,Residues: 1216-1232,'Y',1234-1241,'T',1243-1319,'R',1321-1615,1617-1854 <FUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD---PSHMRGCLQGSSLIIISVFLVGCAQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 NFSRQEVGAATGAVVGGVAGQLFGKGS----GRVSMAIGGAVLGGLIGSKIGQSMDQQDK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -------ĠŚYMDWQKIŚAFVĠĠTLAYĠ--STPDĠGNPPPQĎP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CipA protein - Clostridium thermocellum NyAlternate names: probable cellulosome protein large chain SL Sternate names: probable cellulosome protein large chain SL C;Species: Clostridium thermocellum C;Date: 13.-Jan.-1995 #sequence revision 13.-Jan.-1995 #text_change 01-Dec-2000 C;Accession: S36859; S33527; S25767; S28659; T18261 R;Gerngross, U.T.; Demain, A.L. Submitted to the EMBL Data Library, January 1993 A;Reference number: S36859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 586;
                                                                                                                                                                                                                A Gene: cipC
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-586/Froduct: scaffolding protein CipC #status predicted
F;28-187/Domain: cellulose binding #status predicted <CBD>
F;188-292/Domain: hydrophilic <HYLI>
F;293-439/Domain: hydrophobic <HYBI>
F;440-586/Domain: hydrophobic <HYBI>
                                                                             A;Molecule type: DNA
A;Residues: 1-586 <PAG>
A;Residues: 1-586 <PAG>
A;Cross-references: GB:U40345; NID:g1314291; PID:g1314292
A;Experimental source: ATCC 35319
C;Genetics:
  A;Title: Interaction between the endoglucanase CelA and A;Reference number: PC6006; MUID:96218696; PMID:8636029 A;Accession: PC6006
                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%; Score 249; DB 2;
33.8%; Pred. No. 8.6e-13;
7ative 32; Mismatches 81;
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submitted to the EMBL Data Library, August 1992
A;Reference number: 828659
A;Accession: 828659
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Best Local Similarity
Matches 72; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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C;Species: Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Species: 21-May-1988 #sequence_revision 21-May-1988 #text_change 20-Aug-1999
C;Accession: A25972
R;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabos, T.; McDade, J.E.; Fu, Z.Y.; E
J. Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia rickettsii.
A;Reference number: A25972, MuID:87222152; PMID:3108232
A;Accession: A25972
A;Accession: A25972
A;Resdiues: 1-159 <AND>
A;Resdiues: 1-159 <AND>
A;Cross-references: GB:MI6486; NID:g152467; PIDN:AAA26381.1; PID:g152468
C;Superfamily: rickettsial common antigen
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C;Species: Clostridium cellulolyticum
C;Bace: 17-Aug-1990 #sequence_revision 16-Aug-1996 #text_change 13-Nov-1998
C;Accession: PC6006
R;Pages, S.; Belaich, A.; Tardif, C.; Reverbel-Leroy, C.; Gaudin, C.; Belaich, J. Bacteriol. 178, 2279-2286, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                         Species: Rickettsia typhi
Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
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Best Local Similarity 37.3%; Pred. No. 1e-15;
Matches 60; Conservative 31; Mismatches 54; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
ickettsial common antigen precursor - Rickettsia typhi
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C;ACCESSION: C97012
R;Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A; Bacteriol. 183, 4833-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
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CiSpedies: Clostridium thermocellum
CiSpedies: Clostridium thermocellum
CiSpedies: Clostridium thermocellum
CiSpedies: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
CiAccession: A47704 a47704
A.Title: Gene sequence and properties of Cell, a family E endoglucanase from Clostridium
A;Reference number: A47704; MUID:93171873; PMID:8436949
A;Accession: A47704
A;Accession
                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1483 «KUR>
A;Cross-references: GB:AE001437; PIDN:AAK78886.1; PID:g15023809; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGNSYVDNTSKVTANFVKETASPISTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
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   C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 NGYNYOTITSNVVGTFV-AMDNATATADHYLEISFSNG---
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14.1%; Score 188.5; DB 2;
Best Local Similarity 28.4%; Pred. No. 1.4e-07;
Matches 59; Conservative 20; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.7%; Score 223.5; DB 2; 28.4%; Pred. No. 3.4e-10; iive 22; Mismatches 49;
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EVG-----FGSGAG--TLDDFGGSV----
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C;Species: Clostridium acetobutylicum
                          A;Residues: 1216-1232,'Y',1234-1241,'T',1243-1319,'R',1321-1615,1617-1768,'R',1770-1854
A;Cross-references: EMBL:X67406
R;Fujino, T.; Beguin, P.; Aubert, J.P.
J. Bacteriol. 175, 1891-1899, 1993
                                                                                                                                                                celluloson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scaffolding protein - Clostridium josui
C;Species: Clostridium josui
C;Date: 22-oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T30433
R;Kakiuchi, M.; Isui, A.; Suzuki, K.; Fujino, T.; Fujino, E.; Kimura, T.; Karita, S.; SaJ. Bacteriol. 180, 4303-4308, 1998
A;Title: Cloning and DNA sequencing of the genes encoding Clostridium josui scaffolding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z20837; MUID:98361925; PMID:9696784
A; Accession: T30433
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: L1162 KAK>
A; Kross-references: EMBL:AB004845; NID:93445476; PIDN:BAA32429.1; PID:93445477
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDP--SHMRGCL-QGSSLIIISVFLVGCAQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 SGNNYMDVISKVSGTF-NEVSPAVINADHYLEVALSSDAGSLPAGGSIEIQTRFARNDWS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFSRQEVGAATGAVVGGVAGQLFGKGS----GRVSMAIGGAVLGGLIGSKIGQSMDQQDK 173
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                                                                                                                                                                encoding the
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                                                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: EMBL:X67506; NID:g296879; PID:g296880; PIDN:CAA47840.1; Genetics:
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                                                                                                                                                         A, Title: Organization of a Clostridium thermocellum gene
                                                                                                                                                                                                                         Reference number: Z18847; MUID:93209931; PMID:8458832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.5%; Score 233.5; DB 2; Best Local Similarity 34.0%; Pred. No. 3.8e-11; Matches 66; Conservative 31; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.4%; Score 245; DB 2;
ilarity 51.5%; Pred. No. 7.5e-12;
Conservative 16; Mismatches 30;
                                                                                                                                                                                                               A;Reference number: Z18847; MUID:93209931; PMID:8458
A;Accession: T18261
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DMA
A;Residues: 1821-1854 <FUZ>
A;Cross-references: EMBL:X67506; NID:g296879; PID:g2
C;Genetics:
A;Gene: cipA
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198 -KISPTSISAKQGQ 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 53; Conserv
Molecule type: DNA
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cellulase (EC 3.2.1.4) / cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - Caldocellum s
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A; Residues: 1-915 <SAU>
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                                                                                                                                             NyAlternate names: avicelase I
C;Species: Clostridium stercorarium
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S12021
R;Jauris, S.; Ruecknagel, K.P.; Schwarz, W.H.; Kratzsch, P.; Bronnenmeier, K.; Staudenba
Mol. Gen. Genet. 223, 258-267, 1990
A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoach. A;Reference number: S12021; MUID:91066838; PMID:2250652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yalanse - Caldicellulosiruptor sp.
CyBacies: Caldicellulosiruptor sp.
CyBacies: O2-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
CyBace: O2-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
CyBace: O2-Sep-2000 #sequence_revision 02-Sep-2000
CyBacession: T31085
A;Morris, D.D.; Gibbs, M.D.; Ford, M.; Thomas, J.; Bergquist, P.L.
submitted to the EMBL Data Library, December 1997
A;Bescription: Family 10 and 11 xylanase genes from Caldicellulosiruptor sp. Rt69B.1.
A;Reference number: Z20972
A;Reference number: Z20972
A;Accession: T31085
A;Accession: T31085
A;Accession: T31085
A;Residues: 1-1779 cMOR>
A;Consor-references: EMBL:AF036924; NID:g2760905; PID:g2760909; PIDN:AAB95326.1
C;Genetics:
A;Note: xynC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.1%; Score 188; DB 2; Length 986;
Best Local Similarity 27.6%; Pred. No. 1.8e-07;
Matches 47; Conservative 29; Mismatches 58; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 FSR------QEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     944 FSKADWIDYIQINDYSPSINTSYG-----SNDRITVYISGVLVSGI 984
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                                                                                                  S12021
thermoactive cellulase - Clostridium stercorarium
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------WSNYNQSNDYSFKQACLRQR 868
                                                                                                                                                                                                                                                                                                                                                               A; Accession: S12021
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-986 <JAU>
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Risact, D.C.; Williams, L.C.; Grayling, R.A.; Chamley, L.W.; Love, D.R.; Bergquist, P.L. Appl. Environ. Microbiol. 56, 3117-3124, 1990
A;Title: celB, a gene coding for a bifunctional cellulase from the extreme thermophile "A;Reference number: A43802, MUID:91136262; PMID:2126700
A;Accession: A43802
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce A; Pathway: cellulose degradation C; Superfamily: Streptomyces endo-1,4-beta-xylanase A homology C; Superfamily: Streptomyces endo-1,4-beta-xylanase Agradation C; Keywords: glycosidase; hydrolase; polysaccharide degradation F; 20-320/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 ALLGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 FSRQEVGAATGAVVGGVAGQLF-GKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 QSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DWSNYNQGNDWSW--LQSMTSYGENEKVTAYI----DGVLVWGQE--- 498
N,Alternate names: endo-1,4-beta-glucanase
C;Species: Caldocellum saccharolyticum
C;Date: 30-Jan-1993 #sequence_revision 30-Sep-1993 #text_change 10-Jul-1998
C;Accession: A3802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHA--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----QIRFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%; Score 147; DB 2; Length 915; 23.2%; Pred. No. 0.00042; tive 35; Mismatches 64; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 A-----SNVTFKFVK-LSSSVSGADYYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 ----EIGFKSG-----AGOLOPGKOTGEI---
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Job time : 19:1278 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: BMBL:X13602
C;Function:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 5, 2003, 20:06:36 ; Search time 10.1693 Seconds (without alignments) 1183.846 Million cell updates/sec Run on:

US-09-677-374-6 1335 1 MSVEFYNSNKSAQTNSITPI.....IYGTACPQPDGRWQVISTEK 256 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | P38058     |      | Q52764 rickettsia |            | P22882 rickettsia | P50928 rickettsia |            |            |            |            |            |            | Q02934 clostridium |            |            |            | 4          |            | -          |            |            |           |            |            |            | P55741 escherichia | -          | P10325 haemophilus |            | P29719 paenibacill |            | 9394       | on albomatha Pagago |
|-----------|---------------|------------|------|-------------------|------------|-------------------|-------------------|------------|------------|------------|------------|------------|------------|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|------------|------------|--------------------|------------|--------------------|------------|--------------------|------------|------------|---------------------|
| SUMMARIES |               | CBPA CLOCL |      | 17KD_RICJA        | 17KD_RICCN | 17KD_RICTY        | 17KD_RICAU        | 17KD RICPA | 17KD_RICRH | 17KD RICMO | 17KD_RICAM | CIPB_CLOTM | CIPA_CLOTM | GUNI_CLOTM         | GUNZ_CLOSR | GUX2_CLOSR | 17KD_RICCA | GUNB CALSA | MANB_CALSA | GUNA_CALSA | GUN2_BACSU | GUN3_BACSU | PCP YEREN | YCEA PAELA | GUN1_BACSU | SLYB_SALTY | SLYB_ECOLI         | GUNW ERWCA | PCP HAEIN          | GUNV ERWCA | GUNA_PAELA         | YCFJ_ECOLI | GUNN ERWCA | PMP1 CHLPN          |
|           | มช            | : ר        |      |                   | 159 1      | •                 | 154 1             | 154 1      | 154 1      | 154 1      | 154 1      | 772 1      | 1853 1     | 879 1              | 986 1      | 914 1      | 80 1       | 1039 1     | 1331 1     | 1742 1     | 499 1      | 499 1      | 155 1     | 145 1      | 499 1      | 155 1      | 155 1              | 504 1      | 155 1              | 505 1      | 700 1              | 179 1      | 444 1      | 922 1               |
| di        | ery           | .5.        | 21.6 | 21.4              | 21.3       | 20.7              | 20.1              | 19.4       | 19.4       | 19.2       | 19.1       | 18.4       | 18.4       | 14.1               |            | 12.2       | •          | 10.7       | 10.7       |            | 9.1        | 8.6        |           |            |            |            |                    |            |                    |            |                    | 7.5        |            | 7.3                 |
|           | Score         | ;          | 288  | 286               | 285        | 276.5             | 268               | 259        | 259        | 256        | 255        | 245        | 245        | 188.5              | 188        | 162.5      | 156        | 143.5      | 143.5      | 138.5      | 121        | 115        | 112.5     | 111        | 109.5      | 109        | 104.5              | 103        | 101.5              | 101.5      | 100.5              | 100        | 100        | 98                  |
|           | Result<br>No. |            | 7    | e                 | 4          | ഗ                 | 9                 | 7          | 80         | 6          | 10         | 11         | 12         | 13                 | 14         | 15         | 16         | 17         | 18         | 19         | 20         | 21         | 22        | 23         | 24         | 25         |                    |            | 28                 | 53         | 30                 | 31         | 32         | 33                  |

| P48837 saccharomyc<br>P76572 escherichia<br>P45931 bacillus su<br>P65394 bos taurus<br>P47179 saccharomyc<br>P54867 saccharomyc<br>P54867 saccharomyc<br>P54867 saccharomyc<br>P31348 staphylococ<br>Q02308 drosophila<br>P34308 caenorhabdi<br>P34308 myxococcus<br>P3837723 salmonella |
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| NUS7 YEAST YEGH_ECOLI YQBO_BACSU KICJ_BONIN DAN4_YEAST XWO_BACSU SIG1_YEAST SIEPA_STRAEP HLES_DROME YKR2_CABEL OAR_MYXXA OSMB_SALTY  |
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| 541<br>1585<br>1585<br>1161<br>1332<br>378<br>507<br>1077<br>1061  |
| 7.7.7.00000000000000000000000000000000   |
| 97.5<br>95.90<br>90<br>90<br>90<br>90<br>88<br>87.5<br>87.5  |
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                              143
                                                                                                                      : | | | :
----KVTGYIGGAK--VL 185
 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                   181 EKVKAGQVTR--WRNPDIGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY
                                                 121 ROEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
                                                                           ------KKGQFITIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 396:133-140(1998).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ235273; CAA15258.1; -...
PIR; D33971; D33971.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome. SIGNAL 1 1 1 20 159 17 KDa SURPACE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                  Rickettsia prowazekii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.6%; Score 288; DB 1; Length 159; 37.9%; Pred. No. 3.9e-17;
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20 20 N-ACYL DIGLYCERIDE (PROBAI
159 AA; 16672 MW; A33D404B65EEB071 CRC64;
                                                                                                                             ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP-----
                 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE----
                                                                                                                                                                                                                                                                                      (Rel. 19, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                159 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Madrid E;
MEDLINE=895911; PubMed=2768201;
Anderson B.B., Tzianabos T.;
"Comparative sequence analysis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 171:5199-5201(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-Madrid E;
MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M28482; AAA26378.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                           17 kDa surface antigen precursor.
OMP OR RP833.
                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                       GTACPQPD 246
                                                                                                                                                                               GTA-PGPD 192
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• Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=782;
                                                                                                                                                                                                                                             17KD RICPR
P16624;
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SEQUENCE
 61
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103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                             212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
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                            ---IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Furuya Y., Katayama T., Yoshida Y., Kaiho I.; "Specific amplification of Rickettsia japonica DNA from clinical specimens by PCR." Microbiol. 33:487-489 (1995).
                                                                                                                     64 GAVLGGQIGASMDEQDRRLLELTSQRALESAPSGSNIEWRNPDNGNHGYVTPVRTY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.4%; Score 286; DB 1; Length 159, 37.9%; Pred. No. 5.8e-17; ive 32; Mismatches 52; Indels
                                                                                                                                                                                                             213 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 KOERROQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Last sequence update)
, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequer
01-NOV-1997 (Rel. 35, Last annots
17 kDa surface antigen precursor.
                                                                                        GGLIGSKIGQSMDQQDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Conservative
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia japonica
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                                                                                                                                                                                                                                                                                                                      17KD_RICJA
ID 17KD_RICJA
AC Q52764;
                                                                                          157
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RESULT 4 17KD\_RICCN

9

Gaps

16;

52; Indels

32; Mismatches

Conservative

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anchor (Probable).
             153 1
159 AA;
                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       Rickettsia typhi
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=785;
                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996
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CONFLICT
CONFLICT
SEQUENCE
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                                                  Query Match
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                                                                                                                                                                                                                                                                     RESULT 5
17KD_RICTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=R.rickettsii;
MEDLINE=87222152; PubMed=3108232;
Anderson B.E., Regnery R.L., Carlone G.M., Tzianabos T., McDade J.E.,
Fu Z.Y., Bellini W.J.;
Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia
rickettsii.";
                                                                                                                                                                                                                    "Comparative sequence analysis of a genus-common rickettsial antigen

    Bacteriol. 170:4493-4500(1988).
    SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid

                                                                                                                                                                                                                                                                           SPECIES=R.conorii; STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.;
                                                                                                                                                                                                                                                                                                                                                "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A31836; A31836.
PIR; A33971; A33971.
PIR; B33971; B33971.
PIR; G97860; G97860.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=R.rickettsii;
MEDLINE=89008059; PubMed=1139629;
Anderson B.E., Baumstark B.R., Bellini W.J.;
"Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii: transcription and posttranslational
                                                                                    Rickettsia conorii, and
Rickettsia rickettsii.
Bacternia; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiae.
NCBI_TaxID=781, 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 kDa SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE)
                      01-NOV-1988 (Rel. 09, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 159 AA
                                                                                                                                                                             SPECIES=R.conorii, and R.rickettsii; MEDLINE=89359171; PubMed=2768201;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J03371; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                             . Bacteriol. 171:5199-5201(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 169:2385-2390(1987)
                                                            17 kDa surface antigen precursor
OMP OR RC1287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M28479; AAA26376.1; -.
EMBL; M28400; AAA26376.1; -.
EMBL; AE008675; AAL03825.1; -.
EMBL; M16486; AAA26381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-30 FROM N.A.
STANDARD;
                                                                                                                                                                                                        Anderson B.E., Tzianabos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A25972; A25972.
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modification.";
17KD RICCN
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                                                                                                                                                                                                                                              103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK---I 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 TSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY-----RNSTGQYCREYTQTVVIGGKQ 140
                                                                                                                                                                                                                                                                                                                                                                         157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                               175 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 234
                                                                                                                                                                                                                                                                                                           63
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                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson B.E., Tzianabos T.; "Comparative sequence analysis of a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 171:5199-5201(1989).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                21.3%; Score 285; DB 1; Length 159; 37.9%; Pred. No. 7e-17; tive 31; Mismatches 53; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-ACYL DIGLYCERIDE (PROBABLE).
146 N -> D (IN REF. 3).
153 G -> E (IN REF. 3).
16581 MW; 206A2BBF74FCE169 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 KOERROQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 AA; 16549 MW; 08973E2648FD8CD8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 19, Last sequence update)
(Rel. 34, Last annotation update)
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89359171; PubMed=2768201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 kDa surface antigen precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1991 (Rel. 19, Created)
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                                                                                                                                                                                    61; Conservative
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RESULT 6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pretzman C.I., Stothard D.R., Ralph D., Clark J.B., Fuerst P.A.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
anchor (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Or send d. 17008; AAA82040.1; -. EMBL; U17008; AAA82040.1; -. PROSITE; PS00013; PROKAR LIPOPROTEIN; 1. Outer membrane; Lipoprotein; AAtigen: Signal. SIGNL 20 >154 17 kba SURFACE ANTIGEN. 20 >154 17 kba SURFACE ANTIGEN. N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.4%; Score 259; DB 1; Length 154; 36.5%; Pred. No. 9.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 KOERROQYCREPQOKAMIAGOKOEIYGTACPOPDGR
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
17 kba surface antigen precursor (Fragment).
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PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
OUTCEr membrane; Lipoprotein; Antigen; Signal.
SIGNAL BY SIMILARITY.
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                                                 STRAIN=Maculatum;
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P50931;
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GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTYRNSN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baird R.W., Ross B., Dwyer B.;
Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
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Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=35792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-ACYL DIGLYCERIDE (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 AA; 15967 MW; E3AA833346FAC320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENDL: WILLS FROM LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal.
SIGNAL 1 19 BY SIMILARITY.
CHAIN 20 >154 17 kDa SURFACE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR 248
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                                                                                                                                                                                                                                                                                                                                                                               (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
17 kba surface antigen precursor (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 kDa surface antigen precursor (Fragment)
235 QEIYGTACPOPDGRWQVIS 253
                                                                        141 ÓTTÝGNÁCRÓPDGQWÓVVN 159
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59; Conservative 2
                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsia australis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rickettsia parkeri.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996
                                                                                                                                                                                                                                                                                             17KD_RICAU
P50928;
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P50930;
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57; Conservative
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SEQUENCE FROM N.A.
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NCBI_TaxID=1515;
                                                                                                                  01-OCT-1996 (
01-OCT-1996 (
01-OCT-1996 (
                                                                                      17KD RICAM
P50927;
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                                                                                                                                                                                             SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Ohio 83-441;
Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.2%; Score 256; DB 1; Length 154; 36.5%; Pred. No. 1.7e-14;
17 kDa SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE).
                                                                           Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO00131; PROKKR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

1 19 BY SIMILARIY.

CHAIN 20 > 154 17 KDA SURFACE ANTIGEN.

LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
                                                                        th 19.4%; Score 259; DB 1; Length 15. Similarity 36.5%; Pred. No. 9.8e-15; 57; Conservative 30; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Indels
20 >154 17 kDa SURFACE ANTIGEN.
20 20 N-ACYL DIGLYCERIDE (PROBAL
154 154 AA; 15895 MW; OCF85AD5D96DFEFB CRC64;
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                                                                                                                                                                                                                                                                             213 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR 248
                                                                                                                                                                                                                                                            KOERROOYCREFOOKAMIAGOKOEIYGTACPOPDGR
                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                    154
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Best Local Similarity 36.5
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anchor (Probable).
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20
154 1
154 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=33991;
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SEQUENCE
              LIPID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                          213
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                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 GGLIGSKIGOSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
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01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellulosomal scaffolding protein B (Cellulosomal glycoprotein S1/SL)
(Cellulose integrating protein B) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MO 85-1084;
Stochard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                              Rickettsia amblyommii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=33989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.1%; Score 255; DB 1; Length 154; 36.5%; Pred. No. 2.1e-14; ive 29; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 KOERRQOYCREFQOKAMIAGOKOEIYGTACPOPDGR 248
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                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-CCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
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Cellulosomal scaffolding protein A precursor (Cellulosomal glycoprotein S1/SL) (Cellulose integrating protein A) (Cohesin)
                                   Clostridium thermocellum.
                                                                                                                                       Demain A.L.;
                                                          Clostridium.
                                                                                                                                                                        homology."
                                               Bacteria;
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                                                      Gilbert H.J.;

T "identification of the cellulose-binding domain of the cellulosome subunit S1 from Clostridium thermocellum YS.";

FEMS Microbiol. Lett. 78:181-186(1992).

-!- FUNCTION: ACTG AS A SCAFFOLDING PROTEIN IN THE CELLULOSOME. IT PROMOTES BINDING OF CELLULOSE TO THE CATALYTIC DOMAINS OF THE CELLULOSTRIC ENZYMES PRODABLY THROUGH THE BINDING OF THE REPRATED DOMAINS WITH THE DUPLICATED SEGMENT OF 24 AMINO ACIDS REPERTED DOMAINS WITH THE DUPLICATED SEGMENT OF 24 AMINO ACIDS PRESENT IN CATALYTIC SOUNDINS OF THE CELLULOSOME.

-!- SUBCELLULAR LOCATION: CELL SUBRACE.

-!- DOMAIN: THE COHESIN DOMAINS BIND TO THE DOCKERIN DOMAIN BOY BY THE CATALYTIC COMPONENTS OF THE CELLULOSOME.

-!- SIMILARITY: Contains at least 3 cohesin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
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                                            Poole D.M., Morag E., Lamed R., Bayer E.A., Hazlewood G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGN -- SYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|: || || || || || 340 IGSNGSYNGITSNVKGTFVKMSSS-TNNADTYLEISFTGGTLE 381
                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD001947; CBD 37 1.
PROSITE; PS00018; BF HAND; UNKNOWN 1.
PROSITE; PS0448; CLCGS CELLULOSOME RPT; 2.
Cellulose degradation; Cell wall; Glycoprotein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BBF06DE5E094FE10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COHESIN 1.
LINKER (PRO/THR-RICH).
COHESIN 2.
LINKER (PRO/THR-RICH).
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DOCKERIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOCKERIN 2
                                  MEDLINE=93146373; PubMed=1490597;
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001956; CBD_3.
InterPro; IPR002102; Cohesin.
InterPro; IPR002105; Dockerin.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00942; CBM 3; 1.
Pfam; PF00963; Cohesin; 3.
Pfam; PF00404; Dockerin 1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82491 MW;
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461
607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 772 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIPA CLOTM
Q06851;
01-JUN-1994 (
01-NOV-1997 (
28-FEB-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
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DOMAIN
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Matches
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(Rel. 29, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)

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Tavares G.A., Beguin P., Alzari P.M.;
Tavares G.A., Beguin P., Alzari P.M.;
The crystal structure of a type I cohesin domain at 1.7-A
resolution.";
J. Mol. Biol. 273:701-713(1997).
-!- FUNCTION: ACTS AS A SCAFFOLDING PROTEIN IN THE CELLULOSOME. IT
PROMOTES BINDING OF CELLULOSE TO THE CATALYTIC DOMAINS OF THE
CELLULOLYTIC BRIYMES.
-!- SUBCELLULAR LOCATION: CELL SURFACE.
-!- DOMAIN: THE CHESTY DOMAINS BIND TO THE DOCKERIN DOMAIN BORN BY
C. -!- DOMAIN: THE CHESTY COLDAINS OF THE CELLULOSOME.
-!- SIMILARITY: Contains 2 dockerin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE=93209931; PubMed=8458832; Fujino T., Beguin F., Aubert J.-P.; Noganization of a Clostridium thermocallum gene cluster encoding the "Organization of a Clostridium thermocallum gene clusters encoding the cellulosomal scaffolding protein CipA and a protein possibly involved in attachment of the cellulosome to the cell surface."; J. Bacteriol. 175:1891-1899(1993).
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Shimon L.J.W., Bayer E.A., Morag E., Lamed R., Yaron S., Shoham Y.,
Frolow F.;
                                                                                                                                                                                                                                                                                                                                                                                                              "Sequencing of a Clostridium thermocellum gene (cipA) encoding the cellulosomal SL-protein reveals an unusual degree of internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 368-522.
MEDDINE=97076134; PubMed=8918451;
TOTHO J., Lamed R., Chirino A.J., Morag E., Bayer E.A., Shoham Y.,
Steitz T.A.;
Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Crystal structure of a bacterial family-III cellulose-binding domain: a general mechanism for attachment to cellulose."; EMBO J. 15:5739-5751(1996).
                                                                                                                                                                                                                                                                                                                Gerngross U.T., Romaniec M.P.M., Kobayashi T., Huskisson N.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  structure provides new insights into cellulosome assembly.";
Structure 5:381-390(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A cohesin domain from Clostridium thermocellum: the crystal
                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 29-40 AND 42-43.
STRAIN=ATCC 27405 / DSM 1237;
MEDLINE=93302508; PubMed=8316083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 1213-1361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 184-321.
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EMBL; X67506; CAA47840.1; -.
PIR; S36859; S36859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .. Microbiol. 8:325-334(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE OF 1820-1853 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB; 1ANU; 23-JUL-97.

PDB; 1AOH; 08-JUL-98.

PDB; 1NBC; 26-SEP-98.

ILITEPPO; IPR001956; CBD 3.

ILITERPO; IPR002102; Cohesin.
                                                                                             NCBI_TaxID=1515;
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CELLULOSOMAL SCAFFOLDING PROTEIN A.
COHESIN 1.
COHESIN 2.
LINKER (PRO/THR-RICH).
CELLULOSE-BINDING (BY SIMILARITY).
LINKER (PRO/THR-RICH).
COHESIN 3.
COHESIN 5.
COHESIN 6.
COHESIN 6.
COHESIN 9.
COHESIN 9.
COHESIN 9.
DOCKERIN 1.
DOCKERIN 1.
DOCKERIN 1.
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1196
1361
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369 LKVEFYNSNPSDTINSINPQFKVINIGSSAIDLSKLILRYYYTVDGQKDQTFWCDHA-A1 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 56-69.

STRAIN=NCIB 10682;
XX MEDIARE-93171873; PubMed=8436949;
A Hazlewood G.P., Davidson K., Laurie J.I., Huskisson N.S.,
Gilbert H.J.;
A Gilbert H.J.;
Gilbert 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GUNI CLOTM STANDARD; PRT; 879 AA.

Q02934;

Q1-FEB-1995 (Rel. 31, Created)

01-FEB-1995 (Rel. 31, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Endoglucanase I precursor (EC 3.2.1.4) (EGI) (Endo-1,4-beta-glucanase)

(Cellulase I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium thermocellum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.4%; Score 245; DB 1; Length 1853; 51.5%; Pred. No. 2.5e-12; ive 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1853 AA; 196831 MW; 3ABDDC03ABFC5372 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LGN--SYVDNTSKVTANFVKETASPISTYDTYLDPSHMRGCLQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Conservative
  Query Match
Best Local Similarity
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GUNI_CLOTM
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Matches
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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------EVQIRFSKED 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 NSYVDNTSKVTANFVKETASPISTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFSRQ 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 VEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALLG 62
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MEDLINE-91066838; PubMed-2250652;
Jauris S., Ruecknagel K.P., Schwarz W.H., Kratzsch P.,
Bronnenmeier K., Staudenbauer W.L.;
"Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoactive cellulase (Avicelase I): identification of catalytic and cellulose-binding domains.";
Mol. Gen. Genet. 223:258-267(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Gaps
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01-NOV-1991 (Rel. 20, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Endoglucanase Z precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Thermoactive cellulase) (Avicelase I).
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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CELLULOSE-BINDING (BY SIMIL BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 35A60069A514A927 CRC64;
                                                                                                                                                                                                                                                                                                                      HSSP; P26221, 1TF4.

InterPro; IPR001956; CBD 3.

InterPro; IPR001956; CBD 3.

InterPro; IPR001701; GlyCo_hydro_9.

Pfam; PF00759; CBM 3; 2.

Pram; PF00759; GlyCo_hydro_9; 1.

PROSTIE; PS0059; GLYCOSYL_HYDROL_F9_1; 1.

PROSTIE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.

Cellulose degradation; Hydrolase; GlyCosidase; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.1%; Score 188.5; DB 1; 28.4%; Pred. No. 5.3e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           800 N-----SNVTGNFF-NLSSPKEGADT------CL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 VKAGQVTRWRNPDTGNSYSVEPVRTYQR 210
                                                                                                                                                           entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----WSNYNQSNDYSFKQACLROR
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                                                                                                                                                                                                                                                                                           PIR; A47704; A47704.
HSSP; P26221; 1TF4.
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Matches 59; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGC--LQGSSLIIISVFLVGCAQN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 840 IQIQMFNGNTSDKTNGIMPRYRLTNTGTTPIRLSDVKIRYYYTIDGEKDQNFWCDWSSV-
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                           linkages in cellulose, lichenin and cereal beta-D-glucans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R HSSP; P26221; 1TF4.

R InterPro; IPR001956; CBD 3.

InterPro; IPR001012; DUF291.

R InterPro; IPR001101; Glyco_hydro_9.

R Pfam; PF00942; CBM 3; 2.

R Ffam; PF00759; Glyco_hydro_9; 1.

R Probom; P0001947; CBD 3; 1.

R PROSITE; P800592; GLYCOSYL, HYDROL, F9_1; 1.

R PROSITE; P800699; GLYCOSYL, HYDROL_F9_2; 1.

R PROSITE; P800699; GLYCOSYL, HYDROL_F9_2; 1.

R SIGNAL.

I 25
                                                                                 HYDROLASES).
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1-NOV-1997 (Rel. 35, Last annotation update)
Exoglucanase II precursor (BC 3.2.1.91) (Exocellobiohydrolase II)
(1,4-beta-cellobiohydrolase II) (Avicelase II).
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DOWAIN B.
DOWAIN B.
CELLULOSE-BINDING (BY SIMILARITY).
BY SIMILARITY.
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Clostridium.
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109512 MW; 1802E09B22923690 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 188; DB 1;
; Pred. No. 6.7e-08;
29; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENDOGLUCANASE
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X55299; CAA39010.1; ALT_SEQ. PIR; S12021; S12021.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      986 AA;
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                                                                                                                STRAINCE 11754;
MEDLINE=91364686; PubMed=1909625;
MEDLINE=91364686; PubMed=1909625;
MEDLINE=91364686; PubMed=1909625;
MEDLINE=91364686; PubMed=1909625;
Purification and properties of a novel type of exo-1,4-beta-glucanase (avicelase II) from the cellulolytic thermophile Clostridium stercorarium.";
Eur. J. Biochem. 200:379-385(1991).
-!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages in cellulose and cellotetraose, releasing cellobiose from the non-reducing ends of the chains.
-!- SIMILARITY: BELONGS TO CELLULASE FAMILY L (FAMILY 48 OF GLYCOSYL
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InterPro; IPR001956; CBD 3.
InterPro; IPR001956; GB 3.
InterPro; IPR005102; DUF291.
InterPro; IPR00942; CBM 3: 1.
Pfam; PF00942; CBM 3: 1.
Pfam; PF02011; Glyco_hydro_48; 1.
Pfam; PF02011; Glyco_hydro_48; 1.
ProDom; PD001947; GLHTDRLASE48.
R ProDom; PD010947; GLHTDRLASE48.
R ProDom; PD010943; Glyco_hydro_48; 1.
R ProDom; PD010943; Glyco_hydro_48; 1.
ProDom; PD01094; Glyco_hydro_48; 1.
ProDom; PD01094; Glyco_hydro_H8; 1.
ProDom; PD01094; Glyco_hydro_H8; 1.
SIGNAL 1 33 POTENTIAL.
                                                Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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CHAIN 34 914 EXOGLUCANASE II.

SEQUENCE 914 AA; 103020 MW; DODB6017D6DFF82C CRC64;
Bronnenmeier K., Kundt K., Riedel K., Schwarz W.H., Staudenbauer W.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z69359; CAA93280.1; -. HSSP; Q06851; 1NBC.
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63 NSYVDNTSKVTANFVKETASPTSTYDTYLD 92 셤 ઠે 셤

3 VEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALLG 62

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9; Gaps

Search completed: November 5, 2003, 20:13:26 Job time : 11.1693 secs

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082830 clostridium

Q97794 clostridium Q1208 ricketteia Q31208 ricketteia Q91210 acetivibrio Q9139 clostridium Q46392 clostridium Q46392 clostridium Q9241 bacillu Q9247 caldicellul Q9255 caldicellul Q9250 caldicellul Q9250 caldicellul Q9200 caldicellul Q9200 caldicellul Q9200 caldicellul Q9200 caldicellul Q9200 caldicellul Q9200 caldicellul Q92000 caldibacill

Q8glu7 brucella su Q9hxi3 pseudomonas Q8vue8 brucella ab Q9a8m8 caulobacter Q93tj6 bacillus su Q93ld0 bacillus su Q8yg27 brucella me

O9rfx6 caldibacill

Perfect score:

Sequence:

OM protein

Run on:

Minimum DB Maximum DB

Database

Searched:

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GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
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"Identification of a genus-common Rickettsial surface antigen in the salmonid pathogen Piscirickettsia salmonis.";
submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, AF184152; AAG17000.1; -.
SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piscirickettsia salmonis.
Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
Piscirickettsiaceae; Piscirickettsia.
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64 GAVLGGQIGAGMDEQDRRLAELTSQRALEATPSGTSVEWRNPDNGNHGYVTPNKTY---- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 AELTSQRALEAAPSGSSTEWRNPDNGNYGYVTPNKTY----RNSTGQYCREYTQTVVIG 120
GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 --IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Billings A.N., Teltow G.J., Walker D.H.;
"Molecular characterization of a novel spotted fever group rickettsial species from Ixodes scapularis in Texas.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF031534; AAB95267.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Bertrand D., Hurst G.D.D., Majeus M.B.N.;
"On the evolution of male-killing: Monophyletic origin and horizontal
transfer of male-killing Rickettsia (a-Proteobacteria) from two con-
generic ladybirds, Adalia bipunctata L. and A. decempunctata L.
(Coleoptera: Coccinellidae).",
Submitted (ARR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269517; CAB96383.1; -.
EMBL; AJ269517; CAB96382.1; -.
NON TER 144 144
                                                                                                                                                                                                                                                                                                                                         17 kDa antigen (Fragment).
Rickettsia cooleyi.
Bacternia, Proteobacteria, Alphaproteobacteria, Rickettsiales;
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=69410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17kDA antigen (17 kDa antigen) (Fragment).
male-killing Rickettsia from Adalia bipunctata.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Rickettsiaceae; Rickettsiaceae; Rickettsiaa.
NCBI_TaxID=38028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                            120 -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGLWQVVN 159
                                                                                    KOERROQYCREFOOKAMIAGOKOEIYGTACPOPDGRWOVIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 AA; 14215 MW; A27597A9AFD85FC3 CRC64;
                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.4%; Score 258.5; DB 2
39.3%; Pred. No. 6.3e-14;
tive 25; Mismatches 46
                                                                                                                                                                                                                                        137 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQKQEIYGTACPQPD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 39.3:
nes 53; Conservative
                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDK---IK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 LNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Rickettsia felis: molecular characterization of a new member of the spotted fever group.";
Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
EMBL; AF195118; AAG28452.1; -.
SEQUENCE 159 AA; 16497 MW; 34C5B020AF470A1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bouyer D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L., Zavala-Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
                                                                                                                                                                                                                                                                                                                                            Davis M.J., Ying Z., Brunner B.R., Pantoja A., Ferwerda F.H., Rickettsial relative associated with papaya bunchy top disease."; Curr. Microbiol. 36:80-84(1998).

EMBL, U76907; AAC02809.1; --
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Rickettsia felis (Rickettsia azadi).
Bacteria, Proteobacteria; Alphaproteobacteria, Rickettsiales;
Rickettsiaceae; Rickettsiaee; Rickettsia.
NCBI_TaxID=42862;
                                                                                                                                                                                                                  Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.2%; Score 283; DB 2; Length 159; 37.9%; Pred. No. 7e-16; ive 30; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 AA; 15050 MW; A7AFEEFDE0AEEE4C CRC64;
                                                                             054381;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.7%; Score 303.5; DB 2;
40.1%; Pred. No. 1.3e-17;
iive 30; Mismatches 43;
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MEDLINE=98087556; Pubmed=9425244;
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132 KAYGTACROPDGOWQVV 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 37.9
Matches 61, Conservative
                                                                PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                       NCBI_TaxID=789;
                                                                                                                                                                                              Rickettsia sp.
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120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK---1 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of scaffolding protein CipC and ORFXp, a new cohesin-containing protein in Clostridium cellulolyticum: comparison of various cohesin domains and subcellular localization of ORFXp."; J. Bacteriol. 181:1801-1810(1999).
                                                                                                                      MEDLINE=20575219; PubMed=11133455; Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K., Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K., Schulenburg H.J.G.V.D., Majerus M.E.N.; Incidence of male-killing Rickettsia Spp. (alpha-Proteobacteria) the Ten-Spot Ladybird Beetle Adalia decempunctata L. (Coleoptera: Coccinellidae)."; Appl. Braviron. Microbiol. 67:270-277(2001).

EMBL; AJZ69516; CAB96381.1; -. NON TER
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STRAIN=ATCC 35319;
Reverbel-Leroy C., Tardif C., Belaich A., Bernadac A., Gaudin C.,
Belaich J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium cellulolyticum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Interaction between the endoglucanase CelA and the scaffoldin protein CipC of the Clostridium cellulolyticum cellulosome."; J. Bacteriol. 178:2279-2286(1996).
                                                                                                                                                                                                                                                                                                                                        18.8%; Score 251.5; DB 2; Length 144; 39.4%; Pred. No. 2.6e-13; Live 24; Mismatches 45; Indels 11.
                  male-killing Ricketťsia from Adalia decempunctata.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 35319;
MEDLINE=96218696; PubMed=8636029;
Pages S., Belaich A., Tardif C., Reverbel-Leroy C., Gaudin
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SEQUENCE FROM N.A.
STRAIN=ATCC 35319;
MEDLINE=99173902; PubMed=10074072;
Pages S., Belaich A., Fierobe H.P., Tardif C., Gaudin C.,
Belaich J.P.;
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144 AA; 14801 MW; C825472F16A56AE7 CRC64;
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(TrEMBLrel. 16, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein precursor
                                                                                                                                                                                                                                                                                                                                                                           52; Conservative
17 kDa antigen (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 OKSYGNACROPD 142
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SEQUENCE FROM N.A.
                                                                      NCBI_TaxID=120393;
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Belaich J.P.;
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                                                                          4.
                                                                                                         120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDOODK---I 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 234
                                                                                                                                                                                                           76 TSQRALEAAPSGSNVEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 234
                                                                                                                            10 NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Gaps
                                                                    11;
                                      144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=37816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 137;
                                      Length
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=TT-118;
Billings A.N., Yu X.-J., Teel P.D., Walker D.H.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 14785 MW; C8254739CCA56AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 137 AA; 14167 MW; 75BC1D0D745B428C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          031065; Q9WW02;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
17 kDa antigen (17 kDa protein) (Fragment).
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Last sequence update)
Last annotation update)
                                   ch 18.9%; Score 252.5; DB 2; Il Similarity 39.4%; Pred. No. 2.1e-13; 52; Conservative 24; Mismatches 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AA
                                                                                                                                                                                                                                                                                                                                                                               137 AA
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Q9K4W8;
01-0CT-2000 (TEMBLE1 15,
01-0CT-2000 (TEMBLE1 15,
                                                                                                                                                                                                                                                  235 QEIYGTACPOPD 246
                                                                                                                                                                                                                                                                                    131 ÓKAÝGNÁCRÓPĎ 142
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                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
 144 AA;
                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 TSQRALEAAPSGSSTEWRNPDNGNYGYVTPNKTY-----RNSTGQYCREYTQTVVIGGKQ 123
                                       MEDLINE=22182650, PubMed=12194779,
Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
Genchi C.;
"First detection of spotted fever group rickettsiae in Ixodes ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 18.1%; Score 241.5; DB 2; Length 131; Local Similarity 39.1%; Pred. No. 1.5e-12; Nes 50; Conservative 24; Mismatches 43; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=184232;
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCB TaxID=184231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 AA; 13358 MW; D4152713C9FAA9CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment).
                                                                                                                                                                                          213 KOERROQYCREFQQKAMIAGQKQEIYGTACPQPDGR 248
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EMBL; AJ427883; CAD20879.1; -.
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                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rickettsia sp. IrITA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 QEIYGTAC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 QKAYGNAC 131
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SEQUENCE FROM N.A.
STRAIN=IrITA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                        Q8KLT4;
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208KLT4
AC Q8KLT7
AC Q8KLT7
DT 01-OC
DT 01-NC
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Pages S., Belaich A., Reverbel C., Tardif C., Fierobe H.P., Gaudin C., Bages S., Belaich A., Reverbel C., Tardif C., Fierobe H.P., Gaudin C., Bages S., Belaich D.;
Usubmitted (Or-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; U40345; AAC28899.2; -.
R HSSP; Q06812; NBC.
R InterPro; IPR001105; CBD 3.
R InterPro; IPR001105; CBD 3.
R InterPro; IPR005102; DUP291.
R InterPro; IPR005102; DUP291.
R Ffam; PF00942; CBM 3; 1.
R Ffam; PF00942; CBM 3; 1.
R ProDom; PD001947; CBD 3; 1.
R PRODOM; PD001947; CBD 3; 1.
R PRODOM; PD001947; CBD 3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD---PSHMRGCLQGSSLIIISVFLVGCAQ 117
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"Molecular study and overexpression of the Clostridium cellulolyticum
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MEDLINE=93084757; PubMed=1452660;
MEDLINE=93084757; PubMed=1452660;
MEDLINE=93084757; PubMed=1452660;
MEDLINE=931084757; PubMed=1452660;

"Characterization and comparison of Australian human spotted fever group rickettsiae.";

"Clin. Microbiol. 30:2896-2902(1992).

EMBL; M99391; AAA73386.1; -.

NON_TER 154 154
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.7%; Score 249; DB 2; Length 1546; Best Local Similarity 33.8%; Pred. No. 9.4e-12; Matches 72; Conservative 32; Mismatches 81; Indels 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.3%; Score 244; DB 2; Length 154; ilarity 35.3%; Pred. No. 1.2e-12; Conservative 31; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 27 POTENTIAL.
28 1546 SCAFFOLDING PROTEIN.
1546 AA; 158748 MW; F8651504EC27809F CRC64;
                        celCCF cellulase gene in Escherichia coli.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEMBLrel. 01, Last sequence of 01-OCT-2002 (TrEMBLrel. 22, Last annotation (Clone PRB FISF 1), 5' end CDS (Fragment).
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Matches 55; Conserva
                                                                                        SEQUENCE FROM N.A.
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SIGNAL
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120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 NKQGTGTILIGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Werren J.H., Hurst G.D., Zhang W., Breeuwer J.A., Stouthamer R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.7%; Score 236.5; DB 2; Length 131; 38.3%; Pred. No. .4e-12; tive 24; Mismatches 44; Indels 11
                       17 kDa protein (Fragment).
Rickettsia gp. Callifornia 2.
Bacteria; Proteoacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiaes; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=California 2;
Raoult D.;
"A new SF zickettsia isolated from fleas.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-California 2;
Roux V., Racult D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210693; AAG48554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     131 131
131 AA; 13374 MW; 23C8819B29FFF860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 AA; 13344 MW; AIDCF71050DF52DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.7%; Score 236.5; DB 2; 38.3%; Pred. No. 4e-12; tive 24; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=94117373; PubMed=8288533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beetle (Adalia bipunctata).";
J. Bacteriol. 176:388-394(1994).
EMBL; U04162; AAA19235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 kDa antigen (Fragment).
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Matches 49; Conservative
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01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEIYGTAC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 OKAYGNAC 131
                                                                                                           NCBI_TaxID=147259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsia sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GAVLGGQIVAGMDEQDRRILAELISQRALEAAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                             120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK---1 174
                                                                                                                                                                                                                                                                                                                                                                                                                                     175 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 TSQRALBAAPSGSSTEWRNPDNGNYGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ 123
                                                                                                                                                                                                                                                                                                                                                                       10 NKQGTGTLLGGAGALLGSQFGKGKGQL-VGVGVGAGALLGAVLGGQIGAGMDEQDRRLAEL 68
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Genchi C.,
"First detection of spotted fever group rickettsiae in Ixodes ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria, Alphaproteobacteria, Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35789;
                                                                                                                                                                                                                                                     DB 2; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.9%; Score 239; DB 2; Length 151; Best Local Similarity 35.9%; Pred. No. 3e-12; Matches 55; Conservative 28; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Nilsson K., Pahlson C.;
Nilsson K., Pahlson C.;
Nilsson K., Pahlson C.;
Nilsson K., Pahlson C.;
Submited diagnostic reagent and kit for detection of rickettsiosis.", to the EMBL/GenBank/DDBJ databases.
EMBL, AF181036; AAG09427.1;
NON_TER 151 151 ...
                                                                                                                                                                                                     13358 MW; D4152713C9FAA9CA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 22, Last annotation update)
Outer membrane protein (Fragment).
Rickettsia helvetica.
                                                                                                                                                                                                                                                  Query Match 18.1%; Score 241.5; DB 2; Best Local Similarity 39.1%; Pred. No. 1.5e-12; Matches 50; Conservative 24; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9F0Q1 PRELIMINARY; PRT; 131 AA.
Q9F0Q1, 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQP 245
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                                                                              PRT;
MEDLINE=22182650; PubMed=12194779;
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RESULT 12

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SEQUENCE Query Match

SOCO OCT SOC

RESULT 13 Q9F0Q1 ID Q9F0Q AC Q9F0Q DT 01-MADT 01-MA

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Gaps

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120 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK---I 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 TSQRALEAAPSGSNVEWRNPDNGNYGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genchi C.,
"First detection of spotted fever group rickettsiae in Ixodes ricinus
"First detection of spotted fever group rickettsiae in Ixodes ricinus
from Italy.";
Emerg. Infect. Dis. 8:983-986(2002).
EMBL; AJ427881; CAD20877.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
17.6%; Score 235.5; DB 2; Length 131;
Best Local Similarity 38.3%; Pred. No. 4.9e-12;
Matches 49; Conservative 24; Mismatches 44; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Irital;
MEDLINE=22182650; PubMed=12194779;
Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsia helvetica.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=35789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 AA; 13383 MW; D78C171050CAA9CA CRC64;
                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment).
                                                                                                                                                                                                                                           131 AA.
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                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                        PRELIMINARY;
                                                                       235 QEIYGTAC 242
                                                                                                                   124 OKAYGNAC 131
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SEQUENCE
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Moraxella catarrha Porphorymonas ging Porphorymonas ging PBOMP-2 gene prod Haemophilus influe Novel human diagno

Spider recombinant

Outer surface lipo M catarrhalis MCA1 Moraxella catarrha

Drosophila melanog Drosophila melanog Drosophila melanog H. pylori ORF Olcp A fusion of anti-C Rickettsia rickett

Drosophila melanog Human polypeptide Drosophila melanog Drosophila melanog Drosophila melanog

Total number of

Database

Searched:

Title: Perfect score:

Sequence:

OM protein

Run on

Scoring table:

Streptococcus poly Novel human diagno Streptococcus poly

Streptococcus poly Human prostate can Human nucleic acid Spider silk protei Spider natural sil N.clavipes draglin Nephila clavipes

N. clavipes spider N. gonorrhoeae ami Human polypeptide Human GS930284 pro E. coli expression

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Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimised OspA protein 17E2 amino acid sequence
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/label= B_cell_epitope
                                                                                                                                     AAB82611
ABB6632
ABB66324
ABB61224
AAX11028
AAB10695
ABB61221
ABC63301
ABC63301
ABC63301
ABC63301
ABC66301
ABC66301
ABC67301
ABC67301
ABC67301
AAC6030
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AAR05799
ABG80423
ABG15906
                                                            AAY34487
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 99CA-2281913
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(KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-1999;
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Region
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Bscherichia coli c
C17E2 OspA constru
B. coli codon opti
Piscirickettsia sa
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Piscirickettsia sa
Pseudomonas aerugi
OspA B-cell epitop
                                                                                                     2003, 20:06:21; Search time 29.1969 Seconds (without alignments) 875.264 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq-embl/AA1981.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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                                                                                                                                                                   US-09-677-374-4
832
1 MRGCLQGSSLIIISVFLVGC.....IYGTACPQPDGRWQVISTEK
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              GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
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AAU97868
AABB1128
AAU97869
AAG78025
AAG78025
AAU97867
ABU18820
AABB1130
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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832 832 832 832 815 815 815 127.5

Result Š. Kuzyk MA;

кау мм,

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The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsial salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related Rickettsial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) used in the creation of the vaccine described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
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/label= C17E2_OspA
/note= "Product of OspA gene optimised for expression in
Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct.
                                                                                                                      Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 832; DB 23; Length 161;
100.0%; Pred. No. 3.6e-81;
ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Undefined_N-terminal_fusion_partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RROOYCREFOOKAMIAGOKOEIYGTACPOPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C17E2 OspA construct with N-terminal fusion partner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                Burian J,
                                                                                                                                                                                                                 Example 4; Fig 5; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piscirickettsia salmonis
                  Kay WW,
                                                                                                                                                                          strain, as a vaccine
                                                            WPI; 2002-455221/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 AA;
                                                                                   N-PSDB; ABK52402
                  Thornton JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
AAB81128
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                                                                                                                                                                                                                                                           This invention relates to a method for the protection against infection of a poixilothermic fish by the bacterial pathogen, Piscirickettsia asalmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed 05pA, or an immunogenic fragment of ospA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonis rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents optimised P. salmonis OspA protein 17E2. The DNA encoding OspA 17E2 (AAF86247) has been optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                           Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease; 17e2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 832; DB 22;
100.0%; Pred. No. 3.6e-81;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli codon optimised OspA, 17e2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU97868 standard; Protein; 161 AA
                                                                                                                                                                                                                        Disclosure; Fig 5; 35pp; English
                         Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-2000; 2000US-0677374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-2001; 2001CA-2339327.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piscirickettsia salmonis
                                                                   WPI; 2001-316844/34.
N-PSDB; AAF86247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 161; Conserv
                         Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 AA;
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Sequence

CA2281913-A1.

THORNTON J C.

CA2339327-A1 15-MAR-2002.

Synthetic

AAU97868;

AAU97868 RESULT

121

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셤 Š KAY W W. BURIAN J. KUZYK M A

(THOR/) 1 (KAYW/) 1 (BURI/) 1 (KUZY/) 1

17-MAR-2001.

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Gaps

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The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related rickettsial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) with an N-terminal fusion used in the creation of the vaccine described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                  Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piscirickettsia salmonis; piscirickettsiosis; salmonid rickettsial; septicaemia; SRS; surface antigen; vaccine; antibacterial; fish; ATCC VR-1361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 832; DB 23; Length 256; 100.0%; Pred. No. 6.6e-81; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piscirickettsia salmonis polypeptide P10.6.
                                                                                                                                                                                           Burian J, Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG78025 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 5; 55pp; English.
                                        15-SEP-2000; 2000US-0677374.
19-MAR-2001; 2001CA-2339327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piscirickettsia salmonis.
                                                                                                                                                                                         Kay WW,
                                                                                  THORNTON J C.
                                                                                                                                                                                                                                                                                                                                             strain, as a vaccine
                                                                                                                                                                                                                                    WPI; 2002-455221/49.
N-PSDB; ABK52403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 AA;
                                                                                                                                               KUZYK M A.
                                                                                                                             BURIAN J.
                                                                                                         KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200168865-A2
                                                                                                                                                                                           Thornton JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                  (THOR/)
                                                                                                                             (BURI/) 1
(KUZY/) 1
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                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a method for the protection against infection of a poixllothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed 05pA, or an immunogenic fragment of 0spA in the form of a vaccine. The method is used for protecting animals, particularly poixliothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a P. salmonis OspA construct optimised for expression in Escherichia coli, fused to an undefined N-terminal fusion partner. The fusion protein is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. coli codon optimised OspA, 17e2 with N-terminal fusion peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Outer surface lipoprotein, OspA, antibacterial, immunosupressive, vaccine, poikilothermic fish, fin-fish, Rickettsial septicaemia, Rickettisial disease, 17e2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 832; DB 22; Length 256; 100.0%; Pred. No. 6.6e-81; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RRÓQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU97869 standard; Protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Fig 5; 35pp; English
                    99CA-2281913
                                                              99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 161, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piscirickettsia salmonis
                                                                                                                                                                                                                                      WPI; 2001-316844/34
                                                                                                                                                                                         Burian J,
                                                                                                                          BURIAN J.
KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 AA;
                                                                                                                                                                                                                                                          N-PSDB; AAF86248
                    17-SEP-1999;
                                                            17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA2339327-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU97869;
                                                                                                    (KAYW/)
(BURI/)
(KUZY/)
                                                                                                                                                                                         Kay WW,
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This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA, in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen ic salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents p. salmonis OspA protein. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                      Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piscirickettsia salmonis outer surface lipoprotein OspA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 815; DB 22;
Pred. No. 2.4e-79;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ź
                                                                                                                                                                                                                                                    Example 2; Fig 2B; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU97867 standard; Protein; 162
                                                                                       Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.0%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-2001; 2001CA-2339327.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (THOR/) THORNTON J C. (KAYW/) KAY W W.
                                                                                                                          2001-316844/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                       Burian J,
             (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody response
                                                                                                                                           N-PSDB; AAF86246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                     Кау WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU97867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGLIGSKIGOSMDQDKIKINOSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acid sequences and the encoded protein of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity to protect fish against P. salmonis which causes piscirickettaiosis, also known as salmonid rickettsial septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poikilothermic fish, Piscirickettsia salmonis, rickettsial pathogen, vaccine, OspA, salmonid rickettsial septicaemia, rickettsial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                      New nucleic acids encoding an amino acid sequence homologous to the surface antigen present on Piscirickettsia salmonis are useful to protect fish against piscirickettsiosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                              Simard N, Brouwers H, Jones S, Griffiths S, Valenzuela P;
Burzio L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROOYCREFOOKAMIAGOKOEIYGTACPOPDGRWOVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.0%; Score 815; DB 22; 98.8%; Pred. No. 2.4e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
110..129
/label= B_cell_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OspA antigen amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB81126 standard; Protein; 162
                                                                                                                                                                                                                                                                                                                                                  Claim 6; Fig 5; 25pp; English.
                                                      2000GB-0016080.
2000GB-0016082.
2000GB-0018599.
                                                                                                                            (AQUA-) AQUA HEALTH EURO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99CA-2281913
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                                       2000GB-0005838
   12-MAR-2001; 2001WO-GB01055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.8°
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piscirickettsia salmonis.
                                                                                                                                                                                                                     WPI; 2001-639050/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AA;
                                                                                                                                                                                                                                        N-PSDB; AAH79040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1999;
                                                                       01-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA2281913-A1
                                       11-MAR-2000;
                                                          01-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB81126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Region
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modulating biofilm formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating biofilm formation by bacteria or modulating bacterial antibiotic resistance. The method of the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is afflicted with a biofilm-associated disease or disorder, such as: cystic fibrosis; AIDS; middle ear infections; and medical device-associated infections; and medical device-associated infections. The present amino acid sequence represents a protein that is used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ÓJAGTÁJGÁVÝGGLLÁNQIGGGTGKKIATVAGÁVGGGYAGNKVQEGMQERDTYTTTETRC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a
                                                                                                                                                                                                                                                                             compound capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 QEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGOSMDQQDKI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; antibody.
                                                                                                                                               Identifying compound capable of modulating biofilm formation by bacteria/bacterial antibiotic resistance, useful for treatment of biofilm associated disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 127.5; DB 24; Length 182; Pred. No. 1.8e-05; 13; Mismatches 28; Indels 19;
                                                                                                                                                                                                                                                                                comprises a method for identifying
                                          Greenberg EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 STVHDSSEKVVGYDVKYMLDGKAĞQIRMERDP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 -KLNQSLEKV------KAGQVTRWRNP
                                                                                                                                                                                                                                     Claim 4; Page 152; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
                                          Ś
                                            Lory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OspA B-cell epitope peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AABB1130 standard; Peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.3%;
34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kuzyk MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99CA-2281913.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 34...
Conservative
Thes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piscirickettsia salmonis.
                                          Bangera MG,
(HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-316844/34.
                                                                                     WPI; 2003-075601/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                       N-PSDB; ABT14642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KAYW/) KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA2281913-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1999;
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                                          Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB81130;
                                          Whiteley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB81130
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                        against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in fin-fish against Rickettsial septicaemia and other related Rickettisial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Piscirickettsia salmonis outer surface lipoprotein, OspA, used in the creation of the vaccine described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cystic fibrosis; AIDS; middle ear infection; acne; periodontal disease; catheter-associated infection; medical device-associated infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                      The invention describes a method of protecting a poikilothermic fish
                                                                                                                                                                    Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 815; DB 23; Length 162;
Pred. No. 2.4e-79;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa biofilm formation-related protein #84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biofilm formation modulation; biofilm-associated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 ROQYCREFQOKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                 Kuzyk MA;
                                                                 Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABJ18820 standard; Protein; 182
                                                                                                                                                                                                                                                           Claim 15; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.0%;
Best Local Similarity 98.8%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001; 2001US-285190P.
24-OCT-2001; 2001US-344142P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa
                                                                 Thornton JC, Kay WW,
                                                                                                                                                                                                                     strain, as a vaccine
                                                                                                         2002-455221/49
                    (KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AA;
(BURI/) BURIAN J.
                                                                                                         WPI; 2002-455221/
N-PSDB; ABK52401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200285295-A2
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Sequence

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This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents an immunogenic epitope of the P. salmonis OspA protein. The peptide is used to raise rabbit anti-OspA antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial strain, as a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer surface lipoprotein, OspA, antibacterial, immunosupressive, vaccine; poikilothermic fish, fin-fish, Rickettsial septicaemia;
 vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                     13.5%; Score 112; DB 22; Length 20; 100.0%; Pred. No. 4.7e-05; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer surface lipoprotein OspA based peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burian J, Kuzyk MA;
                                     Example 2; Page 17; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 17; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 109 PVRTYQRYNKQERRQQYCRE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU97871 standard; Peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                         1 PVRTYQRYNKQERRQQYCRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-2001; 2001CA-2339327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-2000; 2000US-0677374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                             20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettisial disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (THOR/) THORNTON J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-455221/49.
                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KUZYK M A.
                                                                                                                                                                                                                                                                         20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thornton JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA2339327-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU97871;
                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BURI/)
(KUZY/)
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                                                                                                                                                                                                                                                                                                                                               Matches
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Gaps

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   to induce immunity
bacterial strain Piscirickettsia salmonis as a vaccine to induce immun:
in fin-fish against Rickettsial septicaemia and other related
Rickettsial diseases caused by either a virus, bacteria or parasite.
This sequence represents a synthetic peptide used to create polyclonal rabbit antibodies against the Piscirickettsia salmonis outer surface
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                       Moraxella, vaccine, respiratory tract infection, antiinflammatory, auditory, antibacterial; otitis media; sinusitis; pneumonia.
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                                                                                                   Length 20
                                                                                                                      Indels
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                                                                                                 13.5%; Score 112; DB 23;
100.0%; Pred. No. 4.7e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                     M catarrhalis MCA100414 protein SEQ ID NO: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ochs M,
                                                                                                                                                                                                                    AAO17565 standard; Protein; 197 AA
                                                                                                                                           109 PVRTYQRYNKQERRQQYCRE 128
                                                                                                                                                           PVRTYQRYNKQERRQQYCRE 20
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                                                                                                  13.5%;
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2000US-228438P
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                                                                                                                                                                                                                                                               (first entry)
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                          Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loosmore S, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-401721/43.
N-PSDB; AAL46497.
                                                                                                           Local Similarity
                                                       lipoprotein, OspA.
                                                                            20 AA;
                                                                                                                                                                                                                                                                                                                                                               WO200218595-A2.
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29-AUG-2000;
29-AUG-2000;
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29-AUG-2000;
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                                                                             Sequence
                                                                                                                                                                                                                                          AA017565;
                                                                                                 Query Match
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29-NOV-2002
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                                                                                                       The present invention provides the protein and coding sequences of proteins from Moraxella catarrhalis. These can be used to produce vaccines which protect against M. catarrhalis infection, which can cause otitis media, respiratory infection, sinusitus, and pneumonia. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                               GVVLLASSMALAGCANTGT --- TGNGTGFGGANVNKAVIGAVAGAL---GGTAISKATGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium, useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia
                                                                                                                                                                                                                                                                                                  7 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVSMAIGG
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of BASB113 protein from Moraxella catarrhalis strain Mc2931 (ATCC 43617), a causative agent of otitis media in children and pneumonia in adulte. The invention provides BASB113 polypeptides, and polymucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB113 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASB113 polypeptide, an immunogenic fragment of a BASB113 polypeptide, or a polypeptide having at least 85% amino acid sequence identity to BASB113, or comprising a
         Moraxella polypeptide and polynucleotides useful as vaccine for immunizing a host e.g. humans against disease e.g. otitis media, pneumonia, caused by infection of the bacteria
                                                                                                                                                                                                                                                                                                                                                                                              61 EKTGRDAILGAAVGAAAGAYMERQAK----QIEQQMQGTGVTVTHDTDTGN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         media; pneumonia; therapy; diagnosis;
                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                ----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN
                                                                                                                                                                                                                                     Length 197;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                  Match 13.3%; Score 111; DB 23; Local Similarity 33.3%; Pred. No. 0.0012; Les 37; Conservative 15; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moraxella catarrhalis BASB113 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB20105 standard; Protein; 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 67; 86pp; English.
                                                                         Fig 9; 277pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASB311; infection; otitis mantibacterial; antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-2000; 2000WO-EP05851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99GB-0015044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                      197 AA
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                                                                         Claim 28;
                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel hyperblebbing Gram-negative bacterium that has been genetically modified by down-regulating expression of Tol genes, and/or attenuating peptidoglycan-binding activity useful for treating bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptidoglycan-binding; peptidoglycan-associated site; outer-membrane; bacterial infection; vesicle-shedding; Bleb; filter sterilised; detergent; deoxycholate; homogeneity; antibacterial; vaccine; roll; roll; ompCD; xompD, PAL-1; PAL-2.
                                                                                                                                                                                                                                                                                                      7 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVSMAIGG
                                                                                                                                                                                                                                                            Gaps
polynucleotide encoding such a polypeptide. A claimed method of diagnosing a Moraxella infection involves identifying a BASB113 polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection comprises at least 1 antibody directed against a BASB113 polypeptide. BASB113 polypeptides also have utility in raising specific antibodies, and in screening for antibacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hyperblebbing; Gram-negative bacterium; genetically modified; Tol
                                                                                                                                                                                                                                                                                                                                                                                     -----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN 103
                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 224;
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                                                                                                                                                                                                                                                          35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thonnard
                                                                                                                                                                                                                ; Score 111; DB 22;
; Pred. No. 0.0014;
15; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moraxella catarrhalis PAL-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 71, 71pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neyt CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG80432 standard; Protein; 224
                                                                                                                                                                                                                   13.3%;
33.3%;
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                                                                                                                                                                                                                                                            37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moraxella catarrhalis.
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                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                           224 AA;
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activity with a vaccine mechanism of action. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease that the property of the propert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX91536 to AAX91801 encode two hundred and sixty six antigenic
Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to
AAY34583. AAX91802 to AAX91989 represent PCR primers used in the
                                                                                                                                                                                                                                                                               8 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSM-AIGGAVLGGLIG
                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                        31;
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                                                                                                                                                                                        Score 102.5; DB Pred. No. 0.011;
                                                                                                                    (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 325-326; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gingivalis protein PG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY34362 standard; Protein; 230 AA
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Webb EA;
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34.7%;
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(first entry)
                                                                                                                                                                                                                          25; Conservative
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                                                                                                                                                                                                                                                                                                                                                   66 ALIGKKMDKQKK
                                                                                                                                                                                                                                                                                                                              67 SKIGQSMDQQDK
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Rothel LJ,
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                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine; antigenic
                                                                                                                                                      223 AA;
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25-AUG-1999
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30-JAN-1998;
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05-MAY-1998;
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29-JUL-1998;
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                                                                                                                                                       Sequence
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                            the use of detergents such as deoxycholate, thus obviating chromatography purification and ultra centrifugation steps. Vesicles prepared from the invention have reduced particle size (allowing sterile filtration through 0.22 mum pores), increased batch homogeneity, and a superior yield. The present amino acid sequence represents a Moraxella catarrhalis protein, as described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
                filter sterilised. The blebs can be made and harvested without
                                                                                                                                                                                                                                                        7 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVSMAIGG
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                          -----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN 103
                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patterson MA;
                                                                                                                                                                                    Length 224;
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                                                                                                                                                                                                                      35; Indels
                                                                                                                                                                                    Score 111; DB 23;
Pred. No. 0.0014;
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Webb EA;
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98AU-0003654.
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98AU-0004963
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(first entry)
                                                                                                                                                                                                                      37; Conservative
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Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-385613/32
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; antigenic
                                                                                                                                                  224 AA
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23-APR-1998;
05-MAY-1998;
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25-AUG-1999
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10-MAR-1998
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gingivitis
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                                                                                                                                                    Sequence
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                                                                                                                                                                                    Query Match
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              readily
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cc activity with a vaccine mechanism of action. The PG polypeptides have antibacterial cc activity with a vaccine mechanism of action. The PG polypeptides can be cc used as vaccines especially against Porphorymonas gingivalis. Probes can cc be used to detect Porphorymonas gingivalis in standard hybridisation cc assays. Porphorymonas gingivalis is involved in periodontal disease cc especially gingivitis.

CC (Updated on 20-MAR-2003 to correct PR field.)

XX
SQ Sequence 230 AA;
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Query Match
Best Local Similarity 34.7%; Pred. No. 0.012;
Matches 25; Conservative 13; Mismatches 31; Indels 3; Gaps 2;

Qy 8 SSLIISTVELVGGAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSM-AIGGAVLGGLIG 66

Db 15 ASVLANALVFAGGGLIA-NMAKGGLIGAGVGAVGANVAGNVAGNVAGNAAGAAGAA 72

67 SKIGQSMDQQDK 78 : ||: ||: | 73 ALIGKKMDKQKK 84

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73 ALIGKKMDKQKK 84

Search completed: November 5, 2003, 20:12:50 Job time: 30.1969 secs

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Sequence 19701, Application US/09252991A

Sequence 19701, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-01-18
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 34.8<sup>1</sup>
Matches 32; Conservative
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US-09-252-991A-19701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22817, A
Sequence 19701, A
                                                                                                                                                5, 2003, 20:11:02; Search time 10.2884 Seconds (without alignments) 662.108 Million cell updates/sec
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832
1 MRGCLQGSSLIIISVFLVGC......IYGTACPQPDGRWQVISTEK 161
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-09-252-991A-23334
US-09-252-991A-23334
US-09-328-352-7802
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US-09-252-991A-28197
US-09-252-991A-28197
US-09-328-352-4253
US-09-328-352-7068
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S-09-252-991A-27926
S-09-107-532A-4748
S-08-556-978B-19
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US-09-034-177-3
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Gaps

19;

4; Length 192; Indels

15.3%; Score 127.5; DB 4; 34.8%; Pred. No. 1.4e-06;

------KAGOVTRWRNP

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RESULT 1
US-09-252-991A-22817
US-09-252-991A-22817
Sequence 22817, Application US/09252991A
Fatent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: MCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: MCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: MSUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: MSUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PRILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                         Sequence 31525, A Sequence 26438, A Sequence 20, Appli Sequence 2, Appli Sequence 1100, Ap Sequence 13, Appl Sequence 23427, A Sequence 23427, A Sequence 27975, A
      US-09-618-869-8

US-09-52-991A-19162

US-09-252-991A-31525

US-09-252-991A-30059

US-09-252-991A-30059

US-09-067-351-2

US-09-360-490-2

US-09-360-490-2

US-08-374-077C-2

US-08-374-077C-2

US-08-374-077C-2

US-08-374-077C-2

US-08-378-378-378-378-378-3

US-07-313-38-378-3

US-09-252-991A-291A-27975

US-09-252-991A-18919
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RESULT 5
US-09-252-991A-31960
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APPLICANT: MAC J. S. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                     45;
                                                                                                                    Length 165;
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                                                                                                                                                     Indels
                                                                                                                   DB 4;
                                                                                                                                                       35;
                                                                                                                 Query Match 13.4%; Score 111.5; DB 4 Best Local Similarity 25.7%; Pred. No. 7.4e-05; Matches 35; Conservative 21; Mismatches 35
                                                                                                                                                                                       5 LOGSSLIIIS----VFLVGC----AQNFSRQE---
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; Sequence 23334, Application US/09252991A
; Patent No. 6551795
; GENERAL INPORMATION:
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                                                                    ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                            --NOSLEKVKAGQVTR 95
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Best Local Similarity 24.1%
Matches 45; Conservative
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NUMBER OF SEQ ID NOS:
SEQ ID NO 19701
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US-09-252-991A-21754
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LENGTH: 306
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APPLICANT: Marc J. Rubenfield et al.

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RESULT 6
US-09-328-352-7802
) Sequence 7802, Application US/09328352
) Setent No. 6562958
) GENERAL INFORMATION:
) APPLICANT: Gary L. Breton et al.
) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
) FILLE REFERENCE: GTC99-03PA
; FILLE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US,09/252,991A

PRIOR PILING DATE: 1999-02-18

PRIOR FILING DATE: US,00/074,788

PRIOR FILING DATE: US,00/094,190

PRIOR FILING DATE: US,00/094,190

NUMBER OF SEQ ID NOS: 33142
     NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 SSILLLSLSLVGSTAFAGDDTRAAIGGALGGVLGSVVGDAVGGSTGAAIGSGIGGAAGGA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 VGAGRGNKTERALGGGLGAAGGNVIGRQIGGSTGGLIGAALGGAGGALGNHYGDGNRRY 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 DOQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 DDDDDYRDRRYYR--RAGYRDGYYRHDNGHHYG----QYKKWKRHKHKHRRY 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92.5; DB 4;
Pred. No. 0.0061;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 99.5; DB 4; Pred. No. 0.0052; 26; Mismatches 4
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTIC
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 23334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31960
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%;
39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         th 12.0%;
| Similarity 22.1%;
| 38; Conservative 26
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Best Local Similarity
Matches 23; Conserv
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4442
LENGTH: 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION AND ACTO SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PELING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43
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                                                                                                                                                                                                                                                                    7 GSSLIIISVFLVGCAQ-----AVVGGVAGQ
                                                                                                                                                                                                                                    4 CLOGSSLIIISVFLVGCAQNFSROEVGAATGAVVGGVAGQLFGKGSGRVSMAIG----
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                                                                                                                                                                                       17;
                                                                                                                                   ch 10.4%; Score 86.5; DB 4; Length 127; 1 Similarity 34.3%; Pred. No. 0.034; 24; Conservative 8; Mismatches 21; Indels 1.
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22.0%; Pred. No. 0.36;
tive 30; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 WKLKVPSSSFNSTQQIDVKAGYALQDQQAE 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4442, Application US/09328352 Patent No. 6562958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Acinetobacter baumannii
US-09-328-352-4442
                                          ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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nes 33; Conserv
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Best Local Similarity
Matches 24; Conserv
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SEQ ID NO 28397
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TYPE: PRT
                        LENGTH:
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Sequence 8009, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BUJMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BUJMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8009
LENGTH: 126
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLS OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLS REPERENCE: 107196.136
CURRENT FILLING DATE: 1999-02-18
PRIOR PILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-07-18
PRIOR FILLING DATE: 1998-07-18
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                -----QDKIKLNQSLEKVK----AGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQ 124
                                                                                                                                                                                                                                                                                                                                       8 SSLIIISVFLVGCAQNF--SRQEVGAATGAVVGGVAGQLFGKGSGR-VSMAIGGAV---- 60
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                                                                                                                                                                                                             11.1%; Score 92.5; DB 4; Length 199; 26.4%; Pred. No. 0.013; tive 19; Mismatches 45; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%; Score 90; DB 4; Length 126; 31.8%; Pred. No. 0.014; tive 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                            34 GAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 YCREFQQKAMIAGQKQEIYG---TACPQ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 VAQQAQ-----APKEQVYGAIASVLPQ 166
CURRENT APPLICATION NUMBER: US/09/328,352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Acinetobacter baumannii
US-09-328-352-8009
                                                                                                               ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7802
                   CURRENT FILLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7802
                                                                                                                                                                                                         Query Match
Best Local Similarity 26.4%
Matches 39; Conservative
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Matches 27; Conservative
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Sequence 6423, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
PAPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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US-09-328-352-7068

US-09-328-352-7068

Sequence 7068, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: UNWBER: US/09/328,352

CURRENT APPLICATION UNWBER: US/09/328,352

CURRENT APPLICATION UNWBER: US/09/328,352

NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 GAATGAVVGGVAGQL-----FGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQ 75
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Pred. No. 0.12;
6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GGIIGAIAGAITNKGS---SMGIIANVVAGLVGSALGQAL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
10.0%; Score 83.5; DB 4;
Best Local Similarity 42.5%; Pred. No. 0.043;
Matches 17; Conservative 9; Mismatches 11;
FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGRAT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REPERRENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEFAN: (781)893-8277
INFORMATION FOR SEQ ID NO: 5149:
SEQUENCE CHARACTERIESTICS:
LENGTH: 84 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...84
SEQUENCE DESCRIPTION: SEQ ID NO: 5149:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Acinetobacter baumannii US-09-328-352-6423
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9.9%;

Best Local Similarity 37.7%;

Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-107-532A-5149
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US-09-328-352-6423
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Ratent No. 6562958
GENERAL INFORMATION:
FAPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4253
LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GSGRVSMAIGGAVLGGLIGSKIGQSMDQ 75
                                                                                                                                                                                       21 AQNFSRQEVGAATGAVVGGVAGQLFGK-----GSGRVSMAIGGAVLGGLIGSKIGQSMDQ 75
                                                                                          DB 4; Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.2%; Score 85; DB 4; Length 258. Best Local Similarity 29.7%; Pred. No. 0.13; Matches 22; Conservative 14; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENČE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                          29;
                                                                                                                  0.64;
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APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: 10-1098
PRIOF APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
                                                                                  Query Match
10.3%; Score 86; DB 4
Best Local Similarity 34.8%; Pred. No. 0.64;
Matches 24; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5149, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PC
OPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 VGAATGAVVGGVAGQLFGK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Acinetobacter baumannii
US-09-328-352-4253
               ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 L-PIKESSFMEKLR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 QDKIKLNQSLEKVK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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925 RSSSTVNGS 933
                                                                                                                                                                                                                                                                                               76 QDKIKLNOS 84
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                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-328-352-4253
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Sequence 6750, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 215
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                                                                                                                                                                    4.
                                                                                                                                                                                                                               113 NDIAQTNNQKD-----YSEDKNLE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 SKIGQSMDQODKIKLNQSLEKVKAGQVTRWRNPDT -- GNSYSVEPVRTYQRYNKQERRQQ 124
                                                                                                                                                                                                         ----- 50
                                                                                                                                                                                                                                                                                     51 -----RVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAG----QVTRWRNP 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.9%; Score 82; DB 4; Length 215;
Best Local Similarity 23.9%; Pred. No. 0.22;
Matches 34; Conservative 22; Mismatches 48; Indels 38; Gaps
                                                                                                                                                                    Gaps
                                                                                                                                                                    35;
                                                                                                                       Query Match

9.9%; Score 82.5; DB 4; Length 217;
Best Local Similarity 25.2%; Pred. No. 0.2;
Matches 36; Conservative 20; Mismatches 52; Indels 3
                                                                                                                                                                                                       5 LOGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSG-
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DD------RYDRRYDRDRR 189
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; SEQ ID NO 7068
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT

ORGANISM: Acinetobacter baumannii
US-09-328-352-6750
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Search completed: November 5, 2003, 20:16:46 Job time : 10.2884 secs

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November 5, 2003, 20:15:12; Search time 18.9085 Seconds (without alignments) 1462.395 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/DSO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644079 segs, 171749292 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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832
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery

No. Score Match Length DB ID

1 832 100.0 256 12 US-10-261-446-4 Sequence 6, Appliant 12 13.5 20 12 US-10-261-446-2 Sequence 6, Appliant 13.5 100.0 256 12 US-10-261-446-2 Sequence 16.9 Appliant 13.5 12 US-10-261-446-1 Sequence 16.9 Appliant 13.5 12 US-10-261-446-1 Sequence 16.9 Appliant 13.5 10.0 423 12 US-10-261-446-1 Sequence 16.9 Appliant 10.0 423 12 US/10/24 Sequence 16.9 Appliant 10.0 423 15 US/10/150 Sequence 9, Appliant 10.0 423 15 US/10/150 Sequence 13.8 Appliant 10.0 423 15 US-10-031-378 Sequence 13.8 Appliant 10.0 423 15 US-10-138 Sequence 13.8 Appliant 10.0 423 15 US-10-29-386-33055 Sequence 14.3 Repliant 10.0 423 15 US-10-29-386-33055 Sequence 14.3 Repliant 10.0 428 12 US-10-244-821-88 Sequence 1, Appliant 10.0 428 12 US-10-444-760-1 Sequence 1, Appliant 10.0 428 12 US-10-244-821-88 Sequence 1, Appliant 10.0 428 12 US-10-444-760-1 Sequence 1, Appliant 10.0 428 12 US-10-444-760-1 Sequence 1, Appliant 10.0 428 12 US-10-244-821-88 Sequence 1, Appliant 10.0 428 12 US-10-444-760-1 Sequence 1, Appliant 10.0 428 12 US-10-444-821 12 US-10-444-82

| 9107               | Sequence 28, Appl | e 28,  | 28,               | 28,  | 28,     | 28,  | 28,  | 28,               | 28,           | 28,     | 28,               | 28,  | 28,    |                   | 28,           | 28,           | 28,               | 28,               | 28,           | 28,               | 28,     | 28,     | 28,               | 28,               | 28,            | 28,               | 4          | 4               |
|--------------------|-------------------|--------|-------------------|------|---------|------|------|-------------------|---------------|---------|-------------------|------|--------|-------------------|---------------|---------------|-------------------|-------------------|---------------|-------------------|---------|---------|-------------------|-------------------|----------------|-------------------|------------|-----------------|
| US-10-156-761-9107 | -09-978-697-28    | 376-60 | US-09-999-832A-28 |      | 39-978- | 978  | -60  | US-09-978-403A-28 | 09-978-564A-2 | -666-60 | US-09-981-915A-28 |      | 09-918 | US-09-978-423A-28 | 09-978-193A-2 | 09-999-830A-2 | US-09-978-757A-28 | US-09-978-187B-28 | 19-978-643A-2 | US-09-978-375A-28 | 09-978- | 09-978- | US-10-143-031A-28 | US-10-002-967A-28 | -10-017-083A-2 | US-10-143-030A-28 | -10-199-67 | US-10-187-749-4 |
| 15                 | 20                | 10     | 10                | 11   | 11      | 11   | 11   | 11                | 11            | 11      | 11                | 11   | 11     | 11                | 11            | 11            | 11                | 11                | 11            | 12                | 12      | 12      | 12                | 12                | 12             | 12                | 12         | 12              |
| 274                | 285               | 285    | 285               | 285  | 285     | 285  | 285  | 285               | 285           | 285     | 285               | 285  | 285    | 285               | 285           | 285           | 285               | 285               | 285           | 285               | 285     | 285     | . 285             | 285               | 285            | 285               | 285        | 285             |
|                    | , o               |        |                   |      |         |      |      |                   |               |         |                   |      | ٠      | 9.3               |               |               |                   |                   |               |                   |         |         | ٠                 |                   |                |                   | ٠          | •               |
| 77.5               | 77.5              | 77.5   | 77.5              | 77.5 | 77.5    | 77.5 | 77.5 | 77.5              | 77.5          | 77.5    | 77.5              | 77.5 | 77.5   | 77.5              | 77.5          | 77.5          | 77.5              | 77.5              | 77.5          | 77.5              | 77.5    | 77.5    | 77.5              | 77.5              | 77.5           | 77.5              | 77.5       | 77.5            |
| 16                 | 18                | 19     | 20                | 21   | 22      | 23   | 24   | 25                | 56            | 27      | 28                | 29   | 30     | 31                | 32            | 33            | 34                | 35                | 36            | 37                | 38      | 39      | 40                | 41                | 42             | 43                | 44         | <b>4</b> 5      |
|                    |                   |        |                   |      |         |      |      |                   |               |         |                   |      |        |                   |               |               |                   |                   |               |                   |         |         |                   |                   |                |                   |            |                 |

## ALIGNMENTS

US-10-261-446-4

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APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Ray, William W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISBASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                           63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
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                                                                                                                                                                                                                                                             3 RGCLQGSSLIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                         2 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ## Sequence 169, Application US/10127032
## Publication No. US20030113742A1
## Sequence 169, Application US/10127032
## Publication No. US20030113742A1
## SERREAL INFORMATION:
## APPLICANT: Bangera, M. Gita
## APPLICANT: Bangera, M. Gita
## APPLICANT: Greenberg, Everett Peter
## APPLICANT: Greenberg, Everett Peter
## TITLE OF INVENTION: ## STORE AND COMPOSITIONS FOR THE MODULATION OF
## TITLE OF INVENTION: ## STORE AND COMPOSITIONS FOR THE MODULATION OF
## TITLE OF INVENTION: ## STORE US 06/285,190
## FILE REPERING DATE: 2002-04-19
## PRIOR PELLING DATE: 2001-04-16
## PRIOR PELLING DATE: 2001-04-16
## PRIOR PELLING DATE: 2001-10-24
## NUMBER OF SEQ ID NOS: 170
## SOFTWARE: FastSEQ for Windows Version 4.0
## SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                 Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.3%; Score 127.5; DB 15; Length 34.8%; Pred. No. 1.8e-05;
tive 13; Mismatches 28; Indels
                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 ROQYCREFOOKAMIAGOKOEIYGTACPOPDGRWQVISTEK 161
                                                                                                           Score 815; DB 12;
Pred. No. 6.8e-78;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 STVHDSSEKVVGYDVKYMLDGKAGQIRMERDP 161
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; TYPE: PRT
; ORGANISM: Piscirickettsia salmonis
US-10-261-446-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                           Query Match
Best Local Similarity 98.8%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 34.55
Local Similarity 34.55
Local Similarity 34.55
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US-10-127-032-169
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                                                                                                                                                                      Sequence 6, Application US/10261446

Publication No. US20030165526A1

GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
APPLICANT: Kuzyk, Milliam W.
APPLICANT: Entrian, Jan
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US 09/677,374
FRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 1099-09-17
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
CORMENDED TO NUMBER: US 60/154,437
NUMBER OF SEQ ID NOS: 20
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Publication No. US20030165526A1

GENERAL INFORMATION:

APPLICANT: Kuzyk, Michael A.

APPLICANT: Kuzyk, Milliam W.

APPLICANT: Ray Milliam W.

APPLICANT: Thornton, Julian C.

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST

TITLE OF INVENTION WUMBER: US/10/261,446

CURRENT APPLICATION NUMBER: US 09/677,374

PRIOR PILING DATE: 2000-09-15

PRIOR PILING DATE: 1999-09-17

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTIN VARIENT NETSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                   121 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 RROQYCREFQOKAMIAGOKQEIYGTACPOPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 832; DB 12; Best Local Similarity 100.0%; Pred. No. 2e-79; Matches 161; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SIGNAL
LOCATION: (-95)..(-1)
US-10-261-446-6
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LENGTH: 162
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121
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, OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- genc
US/10/013,173-8
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US/10/150,762-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 -----SLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREF--QQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 -----SLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREF--QQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 GAATGAVVGGVAGOLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQODKIKLNQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 GAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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APPLICANT: Graves, Scott S.
APPLICANT: Graves, Scott S.
APPLICANT: Schultz, Joanne E.
APPLICANT: Schultz, Joanne E.
APPLICANT: Sanderson, James A.
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 690022.547C2
CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 10.0%; Score 83; DB 15; Length 423; 1 Similarity 21.7%; Pred. No. 2.6; 33; Conservative 24; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.0%; Score 83; DB 15; Length 423; Best Local Similarity 21.7%; Pred. No. 2.6; Matches 33; Conservative 24; Mismatches 67; Indels
                         APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James A.
APPLICANT: Sanderson, James A.
APPLICANT: Reno, Jonh M.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C1
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 69
SOFTWARE: RastSEQ for Windows Version 4.0
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       Schultz, Joanne Elaine
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Publication No. US20030103948A1
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                           SEQ ID NO 8
LENGTH: 423
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US/10/244,821-8
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Sequence 8, Application US/10244821

GENERAL INFORMATION:

APPLICANT: Genbror, Stephen Charles

APPLICANT: Graves, Scott Stoll

APPLICANT: Schultz, Joanne Blaine

APPLICANT: Schultz, Joanne Blaine

APPLICANT: School, James Allen

APPLICANT: Beno, James Allen

APPLICANT: Beno, John M.

APPLICANT: Beno STREPRAYIDIN EXPRESSED GENE FUSIONS AND

ITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

CURRENT APPLICATION NUMBER: US/10/244,821

CURRENT FILING DATE: 2002-09-16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 423
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10.0%; Score 83; DB 12; Length 423;
Best Local Similarity 21.7%; Pred. No. 2.6;
Matches 33; Conservative 24; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                         Indels
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13.5%; Score 112; DB 12;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 20; Conservative 0; Mismatches 0;
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; CURRENT FILING DATE: 2002-09-30; PRIOR APPLICATION NUMBER: US 09/677,374; PRIOR PILING DATE: 2000-09-15; PRIOR FILING DATE: 1999-09-17; NUMBER OF SEQ ID NOS: 20; SOFTWARE: Patentin version 3:0; SEQ ID NO 16; LENGTH: 20
                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                         109 PVRTYORYNKOBRROOYCRE 128
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Publication No. US20030095977A1
GENERAL INFORMATION:
APPLICANT: General Stephen C.
APPLICANT: Graves, Scott Stoll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                             US-10-261-446-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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US/10/013
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Sequence 33055, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANDAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FOR G.
FILLE REFERENCE: ABOMICA-X-2
                     , LOCATION: (562)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1381
                                                                                                                                                                                                                                                                        76 ĠĊFGĠŚŚ----GGYGGLĠĠFGGGSFŔGSYĠSSFGĠSYGĠSFGĠGSFĠGGŚFGGG 131
                                                                                                                                                                                                                                                                                                                                                                        132 GFGGGGFGGGFGGGGGLLSGNEKVTMQNLNDRLASYLDKVRALEESNYELEGKIKE 191
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                                                                                                                                                                                                                                                                                                                           55 AIGGAVLGGLIGSKIGQS---MDQQDKI-----KLNQSLEKVKA-----GQVTR
                                                                                                                                                                                                                        3 GCLQGSSLIIISVF--LVGCAQNFSRQEVGAAT--GAVVGGVAGQLFGKGS-GRVSM---
                                                                                                                                                                        Indels 33; Gaps
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                                                                                                                          Length 618;
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                                                                                                                          DB 10;
                                                                                                                        ch 9.6%; Score 79.5; DE 1 Similarity 28.7%; Pred. No. 9.8; 41; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT ISHIKAWA, UUN
APPLICANT HORIKAWA, HIROSHI
APPLICANT SHIRA, TADAYOSHI
APPLICANT SAKAKI, YOSHIYUKI
APPLICANT SAKAKI, YOSHIYUKI
APPLICANT HATTORI, MASAHIRA
TITLE COF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                                      WRNPDTGNSYSVEPVRTYQRYNK 118
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Publication No. US20030119018A1
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Best Local Similarity
                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: First 71 amino acids of the 17 K antigen of Rickettsia rickettsii
US-10-091-724-5
                                                                                                                                                                                                                                                                                                                              APPLICANT: Ashkar, Samy
TITLE OF INVENTION: Method to Screen Peptide Libraries Using Minicell Display
TITLE OF INVENTION: Method to Screen Peptide Libraries Using Minicell Display
FILE REFERENCE: CMCG 820
CURRENT APPLICATION NUMBER: US/10/091,724
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 06/306,946
PRIOR FILING DATE: 2001-07-20
PRIOR PLING DATE: 2001-07-20
RIOR PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
LOCATION: (524)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equals any of the naturally occurring L-amino acids
191 GSSPKPWIYATSNLASGVPARFSGSGSGTSYSL----TISRVEAEDAATYYCQQWISNPP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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Sequence 1381, Application US/09925300

Patent No. US20020151681A1

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruben,

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAIO1.

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05988

PRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15;
                                                                                                                                                                                                                                   Sequence 5, Application US/10091724
Publication No. US20030105310A1
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
                                                        133 AMIAGQKQEI----YGTACPQPDGRWQVISTE 160
                                                                                                        247 TFGAGTKLELKSSGSGSADPSKDSKAQVSAAE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.9%; Score 82.5; DB Best Local Similarity 32.4%; Pred. No. 0.28; Matches 22; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (507)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ::| :|
GAVLGGQI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGLIGSKI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-925-300-1381
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                                                                                                                                                                                        RESULT 9
US-10-091-724-5
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US-10-414-760-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GARSON, Jean-Pierre
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERNATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6.388-0.365-0
CURRENT APPLICATION NUMBER: US/09/861,597
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: P99/247,806
PRIOR APPLICATION NUMBER: FP 99/01614
PRIOR APPLICATION NUMBER: FP 99/01614
PRIOR APPLICATION NUMBER: P98-02-11
PRIOR PILING DATE: 1998-02-11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 GGGTGGGGGGTGGGGGGTGGGGGGGGGGGGGTVGLPQGVPGGGQDSTALKQTRRPAR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                            30 GAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLBKVK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LFGKGSGRVSMAIGGAVLGG
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                   7,
                                                                                                                                                                                                                                                                                                                                             Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 78.5; DB 9; Length 651;
Pred. No. 13;
4; Mismatches 17; Indels 2
                                                                                                                                                          FEATURE:
OTHER INFORMATION: MAP TO ACOLISS3.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 0.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.0
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
US-10-029-386-33055
                                                                                                                                                                                                                                                                                                                                                                                     Indels
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-112-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
                                                                                                                                                                                                                                                                                                                                         Query Match 9.4%; Score 78.5; DB 12; Best Local Similarity 30.8%; Pred. No. 3; Matches 28; Conservative 12; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 AGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10414760 Publication No. US20030192077A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09861597
Patent No. US20020064539A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 QEVGAATGAVVG----GVAGQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: PHILLIPPE, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 35.37
These 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Nephila clavipes
US-09-861-597-1
                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 LGGQGAGQ 558
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                                                                               SEQ ID NO 33055
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-414-760-1
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491 QGAGAAAAAAVGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAAAGGAGQGG 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 GTSPKLWIYTTSNLASGVPARFSGSGSGTSYSL----TISRMEAEDAATYYCHQRSTYPL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFGKGSGRVSMAIGGAVLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 GAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Goshorn, Stephen Charles
APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Sanderson, James Allen
APPLICANT: Sanderson, James Allen
APPLICANT: Renc, John M.
APPLICANT: Renc, John M.
APPLICANT: REPERENCE: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C3
CURRENT APPLICATION UNMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastESEQ for Windows Version 4.0
SEQ ID NOS
APPLICANT: Yang, Jianjun G.
TITLE OF INVENTION: Production of Silk-Like Proteins in Plants
FILE REFERENCE: BC1014 US NA
CURRENT APPLICATION WUMBER: US/10/414,760
CURRENT FILING DATE: 2003-04-16
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Microsoft Office 97
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 438;
9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 TFGSGTKLELKSSGSGSADPSKDSKAQVSAAE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
9.4%; Score 78.5; DE
Best Local Similarity 35.3%; Pred. No. 13;
Matches 24; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.4%; Score 78; DB 1
21.1%; Pred. No. 9;
tive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 88, Application US/10244821
Publication No. US20030143233A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 QEVGAATGAVVG----GVAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Nephila clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus US-10-244-821-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 LGGQGAGQ 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LIGSKIGQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Search completed: November 5, 2003, 20:27:19 Job time : 18:9085 secs

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                 Copyright
```

 protein search, using sw model OM protein November 5, 2003, 20:10:11; Search time 11.4007 Seconds (without alignments) 1358.089 Million cell updates/sec Run on:

US-09-677-374-4

832 1 MRGCLQGSSLIIISVFLVGC.....IYGTACPQPDGRWQVISTEK 161 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| S         | Description           | rickettsial common | Rickettsial common | Rickettsial common | 17K surface antige | Rickettsial common | 17K antigen precur | conserved hypothet | 17K surface antige | outer membrane lip | conserved hypothet | probable secreted | hypothetical prote | conserved hypothet | lipA protein (impo | probable lipoprote | lipA protein (impo | outer membrane lip |        | outer  |        | ein -  | outer membrane lip | outer membrane pro | PAL cross-reacting | hypothetical prote |        | pz     |      | hypothetical prote |
|-----------|-----------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|------|--------------------|
| SUMMARIES | ID                    | D33971             | B33971             | A33971             | G97860             | C33971             | A25972             | D83169             | AI3418             | S23787             | B83514             | AE0644            | G87629             | B82837             | AD2696             | AF0289             | D97478             | AI0693             | C64921 | F90922 | B85771 | S58234 | AG0443             | AD3350             | 164130             | F87413             | D85674 | H90814 | 48   | H83636             |
|           | DB                    | 7                  | 7                  | ~                  | 7                  | ~                  | 7                  | ~                  | ~                  | N                  | ~                  | ~                 | ~                  | ~                  | ~                  | ~                  | ~                  | ~                  | ~      | ~      | ~      | ~      | ~                  | 7                  | ~                  | ~                  | 7      | 7      | N    | ~                  |
|           | Query<br>Match Length | 159                | 159                | 159                | 159                | 159                | 159                | 182                | 131                | 155                | 154                | 179               | 232                | 257                | 142                | 155                | 125                | 155                | 155    | 155    | 155    | 139    | 155                | 232                | 155                | 257                | 179    | 179    | 179  | 304                |
| a         | Query<br>Match        | 34.6               | 34.3               | 34.3               | 34.3               |                    | 33.2               | 15.3               |                    | ë                  | 13.4               | 13.1              | 13.1               | 13.1               | 12.9               | 12.9               | 12.9               | 12.7               | 'n     | 12.6   | 12.6   | 12.5   | 12.4               | 12.4               | 12.1               | 12.1               | 12.0   | 12.0   | 12.0 | 12.0               |
|           | Score                 | 288                | 285                | 285                | 285                | 276.5              | 276                | 127.5              | 120.5              | 112.5              | 111.5              | 109               | 109                | 109                | 107.5              | 107.5              | 107                | 105.5              | 104.5  | 104.5  | 104.5  | 104    | 103                | 103                | 101                | 100.5              | 100    | 100    | 100  | 99.2               |
|           | Result<br>No.         |                    | 7                  | m                  | 4                  | S                  | 9                  | 7                  | 80                 | σ                  | 10                 | 11                | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18     | 19     | 20     | 21     | 22                 |                    | 24                 | 25                 | 56     | 27     | 28   | <b>5</b> 9         |

| hypothetical prote | probable exported | probable lipoprote | probable outer mem | probable outer mem | hypothetical prote | hypothetical prote | hypothetical prote | glycine-rich prote | porin [imported] - | probable outer mem | hypothetical prote | conserved hypothet | probable tape meas | hypothetical prote | keratin, 54K type |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| D87353             | AC0198            | C82230             | G91049             | D85894             | H65026             | AB3091             | H98195             | T05442             | AI2910             | G97685             | G97672             | AE2897             | F91251             | B82998             | KRBOVI            |
| 332 2              | 179 2             | 223 2              | 172 2              | 172 2              | 172 2              | 278 2              | 278 2              | 608 2              | 220 2              | 220 2              | 100 2              | 100 2              | 691 2              | 137 2              | 526 1             |
| 11.9               | 11.7              | 11.7               | 11.4               | 11.4               | 11.4               | 11.3               | 11.3               | 11.3               | 11.1               | 11.1               | 11.1               | 11.1               | 10.9               | 10.8               | 10.8              |
| 66                 | 97                | 97                 | 95                 | 95                 | 95                 | 94                 | 94                 | 94                 | 92.5               | 92.5               | 92                 | 92                 | 90.5               | 90                 | 90                |
| 30                 | 31                | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                |

## ALIGNMENTS

| - |   |  |
|---|---|--|
| H | - |  |
| 迼 | 5 |  |

rickettsial common antigen precursor - Rickettsia prowazekii
NyAlternate names: 17kD surface antigen; outer membrane protein (omp); RP833
C;Species: Rickettelala prowazekii
C;Date: 16-Mar-1990 #text\_change 03-Nov-2000
C;Accession: D33971; B71645
R;Anderson, B.E; Tzianabos, T.
R,Anderson, B.E; Tzianabos, T.
Bacteriol. 171, 5199-5201, 1389
A;Fitle: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A33971; MUID:89359171; PMID:2768201

A; Accession: D33971

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-159 <AND>

A;Cross-references: GB:M28482; NID:g152461
A;Note: the sequence in GenBank entry RIRANT17KC, release 109.0, (PID:g152462) omits the A;Note: the sequence in GenBank entry RIRANT17KC, release 109.0, (PID:g152462) omits the Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893

A; Accession: B71645

A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

C; Superfamily: rickettsial common antigen C; Keywords: surface antigen A; Gene: omp; RP833

16; Length 159; 52; Indels Query Match
Best Local Similarity 37.9%; Pred. No. 1.6e-18;
Matches 61; Conservative 32; Mismatches 52.

9

Gaps

63 61 8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL ઠે 셤

62 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117 δ

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118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158 ઠે

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B33971 Rickettsial common antigen precursor - Rickettsia conorii

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141 QTTYGNACRQPDGQWQVVN 159
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Best Local Similarity
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C;Species: Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Species: Rickettsia rickettsii
S;Anderson, B.E.; Tzianabos, T
J; Bacteriol. 171, 5199-5201, 1989
A;Anderson, B.E.; Tzianabos, T
A;Accession: A33971; MUID:89359171; PMID:2768201
A;Accession: A33971
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A;Accession: A33971
A;Accession: A33971
C;Species: Rickettsia conorii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C;Accession: B3397:
J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A33971; MUID:89359171; PMID:2768201
A;Reference number: A33971
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <AND
A;Residues: 1-159 <AND
A;Residues: GB:M28479; NID:g152463; PIDN:AAA26379.1; PID:g152464
C;Superfamily: rickettsial common antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 GAVLGGOIGAGMDEODRRLAELTSORALETAPSGSNVEWRNPDNGNYGYVTPNKTY--- 119
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     34.3%; Score 285; DB 2; Length 159;
1 Similarity 37.9%; Pred. No. 3e-18;
61; Conservative 31; Mismatches 53; Indels
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-RNSTGQYCREYIQIVVIGGKQQKAYGNACRQPDGQWQVVN 159
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Best Local Similarity 37.9%; Pred. No. 3e:18;
Matches 61; Conservative 31; Mismatches 1
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Best Local Similarity
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C,Accession: A25972
R;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabos, T.; McDade, J.E.; Fu, Z.Y.; E
Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia rickettsii
A;Reference number: A25972; MUID:87222152; PMID:3108232
A;Accession: A25972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Anderson, B.E.; Tzianabos, T.
2. Bacteriol. 171, 5199-5201, 1989-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A33971; MUID:89359171; PMID:2768201
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893 A;Accession: G97860 A;Accession: G97860 A;Etatus: preliminary A;Molecule type: DNA A;Residues: 1-159 <KUR>
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                                                                                                                                                                                             A;Cross-references: GB:AE006914; PIDN:AAL03825.1; PID:g15620425; GSPDB:GN00173
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERROQYCREFQQKAMIAGQK 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsial common antigen precursor - Rickettsia typhi
C;Species: Rickettsia typhi
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17K antigen precursor - Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 20-Aug-1999
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A;Residues: 1-159 cAND.
A;Cross-references: GB:M26481; NID:g152459; PIDN:AAA26377.1; PID:g152460
C;Superfamily: rickettsial common antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                       34.3%; Score 285; DB 2; 37.9%; Pred. No. 3e-18; ative 31; Mismatches 53.
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C,Superfamily: rickettsial common antigen
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Thu Nov

us-09-677-374-4.rpr

Gaps

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outer membrane lipoprotein precursor - Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 29-Sep-1999
C;Accession: S23787
R;Bacumler, A.J.; Hantke, K.
J. Bacteriol. 174, 1029-1035, 1992
A;Title: A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine uptake in Esc
A;Reference number: S23786; MUID:92121089; PMID:1732192
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Cispecies: Fseudomonas aeruginosa
Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
CiAccession: B83514
Ristover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Ristover, C.K.; Pham, X.Q.; Brwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82956; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE004537; GB:AE004091; NID:g9946960; PIDN:AAG04442.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein PA1053 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                    92 QVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGTACPQPD 151
                                                                                                                                                                                                                                                                                                                                                                                                     67 GAVLGGFLGNTVGGGTGRSLATAAGAVAGGMAGQGVQGAMNRTDGVQLEVRKDDGTTILV 126
                                                                                                                                                                                                                                                                                                            14 GKGSGFPS--LGGSSQKPETNLLASLGNGLFGNSASQLSAADRRKALEAEYRALEYSPAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AVAIAAVTLIGCANNNILSGDVFSASQAKQVQTVIYGILLSVRPVIIQGGDDNNVMGAIG
                                                                                                                                                                                                                                                      46 GKGSGRVSMAIGG-----AVLG-GLIGSKIGQ--SMDQQDKIKLN-QSLEKVKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X60448; NID:g48577; PIDN:CAA42977.1; PID:g48579
C;Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                     14.5%; Score 120.5; DB 2; Length 131; 31.7%; Pred. No. 0.0011; ive 17; Mismatches 44; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 112.5; DB 2
; Pred. No. 0.0067;
19; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 -- NOSLEKVKAGQVTRWRNPDTGNSYSVEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 VQKQGPTRFSVGQ--RVMLASSGSTVTVSP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 SLIIISVFLVGCAQN-----FSRQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.5%;
24.7%;
A; Experimental source: strain 16M
                                                                                                                                           Query Match
Best Local Similarity 31.7*
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 37; Conserv
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A;Molecule type: DNA
A;Residues: 1-154 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-155 < BAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 GRW 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 GSW 127
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                                                  A; Map position: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                             C, Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein PA3819 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Species: Ds-sep-2000 #sequence_revision 15-Sep-2000 #text_change 01-Mar-2002 C;Accession: D83169 B S;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Bracdy, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: D83169 A;Status: preliminary A;Molecule: Lype: DNA A;Residues: L182 <STO> A;Cross-references: GB:AE004799; GB:AE004091; NID:g9949981; PIDN:AAG07206.1; GSPDB:GN001 A;Residues: L-182 <STO> A;Cross-references: Etrain PA01 C;Genetics: A;Gene: PA3819 C;Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tr. surface antigen precursor [imported] - Brucella melitensis (strain 16M)
['Species: Brucella melitensis
['Species: Brucella melitensis
['Species: Brucella melitensis
['Species: Ol-Peb-2002 #sequence_revision 01-Peb-2002 #text_change 01-Peb-2002
['Accession: A1348
['Spelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
A;Rolccule type: DNA
A;Residues: 1-131 < KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52516.1; PID:g17983328; GSPDB:GN00190
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                                                                                                                                                                                                                                                                                                                                                                       GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                       8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 QEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKI-----
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                                                                                                                                                                                                       Gaps
                          A,Residues: 1-159 <AND>
A,Cross-references: GB:M16486; NID:g152467; PIDN:AAA26381.1; PID:g152468
C,Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                    16;
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                                                                                                                                              Length 159;
                                                                                                                                           Query Match 33.2%; Score 276; DB 2; Length 15: Best Local Similarity 37.3%; Pred. No. 1.9e-17; Matches 60; Conservative 31; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 STVHDSSEKVVGYDVKYMLDGKAĞQIRMERDP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 -KLINOSLEKV-
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Matches
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4

Gaps

51;

99

81

--- VGAAT 33

73

16;

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A;Accession: G87629
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-232 <STO>
A;Cross-references: GB:AE005673; NID:g13424723; PIDN:AAK25035.1; GSPDB:GN00148
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 LVGCAQNFSRQEVGAATGAVVGGVAGQLFGK---GSGRVSMAIGGAVLGGLIGSKIGQSM
                                                                                                                                                                                                                                                                                                                        13.1%; Score 109; DB 2; Length 232; 33.7%; Pred. No. 0.021; ive 14; Mismatches 33; Indels
A; Reference number: A87249; MUID:21173698; PMID:11259647
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Best Local Similarity 47.5%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 DOODKIKINOS
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 32; Conserv
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AD2696
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: G87629
R;Accession: G87629
R;Aiceman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
M. J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable secreted protein STY1252 [imported] - Salmonella enterica subsp. enterica serov C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #sequence_revision 09-Nov-2001
                                                                                                                                                                                                                                                               4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 GAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVK 89
                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 VGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL-----
                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 GSVLGAVAGGVIGHQFGGGRGKDVATVVGALGGGYAGNQIQGSMQESD
                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                      Score 111.5; DB 2;
Pred. No. 0.0082;
                                                                                                                                                                                                                                                                                                                                   5 LQGSSLIIIS----VFLVGC-----AQNFSRQE-
                                                                                                                                                                                    ch 13.4%; Score 111.5; I Similarity 25.7%; Pred. No. 0.006
35; Conservative 21; Mismatches
                                 C,Genetics:
A,Gene: PA1053
C,Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 STRAYVOQVDQGQIFR 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable secreted protein STY1252
C;Species: Salmonella enterica sub
       source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --NOSLEKVKAGOVTR 95
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                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 35; Conserv
       A; Experimental
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Conserved hypothetical protein XF0178 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: B82837
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-257 <SIM
A;Residues: 1-257 <SIM
B;Correr, B:Correr, B:C.; Arruda, P.; Abreu, F.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, HI
B;Simpson, A.J.G.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, HI
B=Neto, E.; Doceona, C.; BI-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, W.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, B.E.; Laigri
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.,
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, E.C.; Palmieri, D.A.;Authors: de Silva, A.C.R.; da Silva, R.C.; Santelli, R.V.; Sawasak, A.A.,Authors: da Silva, A.C.R.; da Silva, R.N.; Silva, D.C., W.A.; da Silvain, D.A., Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
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C;Species: Agrobacterium tumefaciens
C;Date: 11.-Jan.-2002 #sequence_revision 11.-Jan.-2002 #text_change 18-Nov-2002
C;Accession: AD2696
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
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Pred. No. 0.024;
9; Mismatches 12; Indels
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probable lipoprotein slyB [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AF0289
R;Parkhill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. & deno-Tarragg, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Simmonds, M.; Skelton, J.; Stevens, R.M.; Davis, P.; Dougan, G.; A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Title: Genome sequence of Yersinia pestis, pMID:11586360
A;Accession: AF0289
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-155 <KUR>
A;Residues: 1-155 <KUR>
A;CGenetics:
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2656
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Goserreferences: GB:AE008688; PIDN:AAL41986.1; PID:g17739358; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
A;Gonetics:
A;Genetics:
A;Amp position: circular chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 SGVELDRGDQTKALEAEYKALETAPVGTPVIWTGDDVKGQVVANAP---YQVGN----- 107
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C,Superfamily: PAL cross-reacting lipoprotein
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Job time: 11.4007 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 5, 2003, 20:06:36 ; Search time 6.39551 Seconds (without alignments) 1183.846 Million cell updates/sec Run on:

US-09-677-374-4 832 1 MRGCLQGSSLIIISVFLVGC......IYGTACPQPDGRWQVISTEK 161 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

|           |        | Description  |            |            | ~          |            |            |            |            | 6          | 7          |            | ~         |            | -             |           | -          |            | P06394 bos taurus |            | P45931 bacillus su |            |            | escheri    | 0          | m          |      | _          | Q8z460 salmonella | Q9z158 rattus norv | plue      | P26011 mus musculu |            | Q9kxp9 streptomyce |            |
|-----------|--------|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|---------------|-----------|------------|------------|-------------------|------------|--------------------|------------|------------|------------|------------|------------|------|------------|-------------------|--------------------|-----------|--------------------|------------|--------------------|------------|
| SUMMARIES |        | ΙD           | 17KD RICPR | 17KD_RICJA | 17KD_RICCN | 17KD_RICTY | 17KD_RICAU | 17KD_RICPA | 17KD RICRH | 17KD RICMO | 17KD_RICAM | 17KD RICCA | PCP YEREN | SLYB_SALTY | SLYB_ECOLI    | PCP HABIN | YCFJ ECOLI | YFGH_ECOLI | K1CJ BOVIN        | XKDO BACSU | YOBO BACSU         | YKR2 CAEEL | OSMB SALTY | OSMB_ECOLI | KRE2_CANAL | CYSH SALTY |      | Y615_AQUAE | CYSH SALTI        | STXG RAT           | VP5 BTV11 |                    | CANS_BOVIN | SYA_STRCO          | K1CJ_HUMAN |
|           |        | DB           | -          | н          | Н          | Н          |            |            | н          | Н          | Н          | Н          | Н         | н          | <del></del> 1 | -4        | н          | -          | -                 | -          | н                  | -          | ٦          | Н          | Н          | Н          | Н    | Н          | -                 | -                  | Н         | -1                 | н          | -                  | -          |
|           |        | Match Length | 159        | 159        | 159        | 159        | 154        | 154        | 154        | 154        | 154        | 80         | 155       | 155        | 155           | 155       | 179        | 172        | 526               | 1332       | 1585               | 783        | 72         | 72         | 431        | 243        | 541  | 132        | 243               | 301                | 526       | 806                | 263        | 890                | . 593      |
| •         | ouery  | Match        |            | 34.4       | 34.3       | 33.2       | 32.2       | 31.1       | 31.1       | 30.8       | 30.6       | 18.8       | 13.5      | 12.7       | 12.6          | 12.1      | 12.0       | 11.4       | 10.8              | ö          | 10.6               | 10.5       | 10.4       |            |            | •          |      |            |                   |                    |           | 9.6                | 9.6        | 9.6                | 9.5        |
|           |        | Score        |            | 286        | 285        | 276.5      | 268        | 259        | 259        | 256        | 255        | 156        | 112.5     | 105.5      | 104.5         | 101       | 100        | 95         | 90                | 90         | 88                 | 87.5       | 86.5       | 85.5       | 84.5       | 82.5       | 82.5 | 82         | 81.5              | 81.5               | 81.5      | 80                 | 79.5       | σ                  | 79         |
|           | Result | No.          | 1          | ~          | ٣          | 4          | S          | 9          | 7          | œ          | σ          | 10         | 11        | 12         | 13            | 14        | 15         | 16         | 17                | 18         | 19                 | 20         | 21         | 22         | 23         | 24         | 25   | 26         | 27                | 28                 | 29        | 30                 | 31         | 32                 | 33         |

| 34                     | 78.5 | 9.4 | 219 | ч | YIAD ECOLI | P37665 | escherichia |
|------------------------|------|-----|-----|---|------------|--------|-------------|
| 35                     | 78.5 | 9.4 | 747 | н | SPD1_NEPCL | P19837 | nephila cla |
| 36                     | 78   | 9.4 | 514 | н | ATPA_THIFE | P41167 | thiobacillu |
| 37                     | 77.5 | 9.3 | 359 | н | ATPA_BOVIN | P19482 | bos taurus  |
| 38                     | 77.5 | 9.3 | 467 | ч | HEM1 MYCLE | P46724 | mycobacteri |
| 39                     | 77.5 | 9.3 | 543 | ч | ATPA_RAT   | P15999 |             |
| 40                     | 77.5 | 9.3 | 553 | Н | ATPA_HUMAN | P25705 | homo sapien |
| 41                     | 77   | 9.3 | 266 | ч | CANS RABIT | P06813 | _           |
| 42                     | 76.5 | 9.5 | 553 | - | ATP0_BOVIN | P19483 | bos taurus  |
| 43                     | 76.5 | 9.5 | 553 | - | ATPA_MOUSE | 003265 | mus musculu |
| 44                     | 76.5 | 9.5 | 269 | н | K1CJ_MOUSE | P02535 | mus musculu |
| 45                     | 76.5 | 9.5 | 727 | 1 | IF2M_HUMAN | P46199 | homo sapien |
|                        |      |     |     |   |            |        |             |
|                        |      |     |     |   | ALIGNMENTS |        |             |
|                        |      |     |     |   |            |        |             |
| RESULT 1<br>17KD_RICPR | ĸ    |     |     |   | ;          |        |             |

| PR STANDARD;  990 (Rel. 15, Created 991 (Rel. 19), Last se 1001 (Rel. 19), Last se 1001 (Rel. 19), Last se 1001 (Rel. 19), Last se 11 proceobacteria; Alp 12 proceobacteria; Alp 13 proceobacteria; Alp 13 proceobacteria; Alp 13 proceobacteria; Alp 13 proceobacteria; Alp 13 proceobacteria; Alp 13 proceobacteria; Alp 13 proceobacteria; Alp 13 proceobacteria; Alp 13 proceobacteria; Alp 13 proceobacteria; Alp 13 proceobacteria; Alp 14 proceobacteria; Alp 15 proceobacteria; Alp 16 proceobacteria; Alp 17 proceobacteria; Alp 18 proceobacteria; Alp 18 proceobacteria; Alp 19 proceopacteria; Alp 19 proceopacteria; Alp 19 proceopacteria; Alp 10 proceopacteria; Alp 10 proceopacteria; Alp 11 proceopacteria; Alp 12 proceopacteria; Alp 13 proceopacteria; Alp 13 proceopacteria; Alp 15 proceopacteria; Alp 16 proceopacteria; Alp 18 proceopacteria; Alp 19 proceopacteria; Alp 19 proceopacteria; Alp 19 proceopacteria; Alp 10 proceopacteria; Alp 10 proceopacteria; Alp 11 proceopacteria; Alp 12 proceopacteria; Alp 13 proceopacteria; Alp 15 proceopacteria; Alp 16 proceopacteria; Alp 16 proceopacteria; Alp 18 proceopacteria; Alp 18 proceopacteria; Alp 19 proceopacteria; Alp 19 proceopacteria; Alp 10 proceopacteria; Alp 10 proceopacteria; Alp 10 proceopacteria; Alp 10 proceopacteria; Alp 11 proceopacteria; Alp 12 proceopacteria; Alp 13 proceopacteria; Alp 14 proceopacteria; Alp 15 proceopacteria; Alp 16 proceopacteria; Alp 16 proceopacteria; Alp 16 proceopacteria; Alp 17 proceopacteria; Alp 18 pro | Best Local Similarity 37.9%; Pred. No. 3.9e-18;<br>Matches 61; Conservative 32; Mismatches 52; Indels 16; Gaps 6; |
|--|---|
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"Comparative sequence analysis of a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                      Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
                   01-NOV-1988 (Rel. 09, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                 Rickettsiaceae, Rickettsieae, Rickettsia.
NCBL_TaxID=781, 783;
                                                                                                                                                                                                                                                                                                        SPECIES=R.conorii, and R.rickettsii;
MEDLINE=89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIES=R.conorii; STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
                                                               28-FEB-2003 (Rel. 41, Last annota
17 kDa surface antigen precursor.
OMP OR RC1287.
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 171:5199-5201(1989)
                                                                                                                                          Rickettsia conorii, and Rickettsia rickettsii.
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modification.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Racult D.;
                                                                                                                                                                                                                                                                                                                                                                                                          gene.
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                         | ::| :|| || || :|| : || GAVLGGQIGASMDEQDRELLELTSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                               GGLIGSKIGOSMDOODK----IKLNOSLEKVKAGOVTRWRNPDTGNSYSVEPVRTYORYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=YH;
MEDLINE=95229950; PubMed=7714214;
MEDLINE=95229950; PubMed=7714214;
Furuya Y., Katayama T., Yoshida Y., Kaiho I.;
Furuya Y., Katayama T., Yoshida Y., Kaiho I.;
Farific amplification of Rickettsia japonica DNA from clinical specimens by PCR.;
J. Clin. Microbiol. 33:487-489(1995).
-: SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales, Rickettsiaceae, Rickettsiaceae, Rickettsia.
NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.4%; Score 286; DB 1; Length 159; 37.9%; Pred. No. 5.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

SIGNAL

1 19 BY SIMILARITY.

CHAIN

20 159 17 KDa SURFACE ANTIGEN.

LIPID

20 N-ACYL DIGLYCERIDE (PROBABLE).

SEQUENCE 159 AA; 16554 MW, CDDCE7CEBDCD6B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
                                                                                                                                                                                        118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                                                                                                                                 : |||||: | :||:||: | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 kDa surface antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D16515; BAA03965.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                       17KD RICJA
                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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SPECIES=R.rickettsii;
MEDLINE=87222152; PubMed=3108232;
Anderson B.E., Regnery R.L., Carlone G.M., Tzianabos T., McDade J.E.,
Fu Z.Y., Bellini W.J.;
                                                                                                                                 "Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 170:4493-4500(1988).

-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; B33971; B33971.
PIR; G97860, G97860.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                             SPECIES=R.rickettsii;
MEDLINE=89008059; PubMed=3139629;
Anderson B.E., Baumstark B.R., Bellini W.J.;
"Expression of the gene encoding the 17-kilodalton antigen from
Rickettsia rickettsii: transcription and posttranslational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 kDa SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE)
N -> D (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ымы, J03371; -; NOT_ANNOTATED_CDS.
PIR; A25972; A25972.
PIR; A31836; A31836.
PIR; A33971; A33971.
                                                                                                                                                                         rickettsii.";
J. Bacteriol, 169:2385-2390(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE008675; AAL03825.1; -. EMBL; M16486; AAA26381.1; -. EMBL; J03371; -; NOT ANNOTATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M28479; AAA26379.1; -. EMBL; M28480; AAA26376.1; -.
                                                                                                                                                                                                                                                                      SEQUENCE OF 1-30 FROM N.A.
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141 QTTYGNACRQPDGQWQVVN 159
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                     64 GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                            62 GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
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                                                                                                                                                     8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
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Rickettsiaceae, Rickettsieae, Rickettsia.
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                                                             34.3%; Score 285; DB 1; Length 159; 37.9%; Pred. No. 7e-18;
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20 20 N-ACYL DIGLYCERIDE (PROBABLE)
159 AA; 16549 MW; 08973E2648FD8CD8 CRC64;
                                                                                                           Indels
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G -> E (IN REF. 3).
; 206A2BBF74FCE169 CRC64;
                                                                                                                                                                                                                                                                                                                                                       120 -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
                                                                                                                                                                                                                                                                                                                                 118 KOERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 33.2%; Score 276.5; DB 1; Similarity 39.6%; Pred. No. 3.8e-17; 55; Conservative 27; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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                                                                                                         31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; C33971; C33971.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 kDa surface antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 171:5199-5201(1989)
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                    16581 MW;
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                                                                                                         61; Conservative
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153 1
159 AA;
                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia typhi
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CONFLICT
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKIMIIALAASMLQACNSPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
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                                                                                                                                                                                                                                                                                                                                                                                            Baird R.W., Ross B., Dwyer B.;
Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 268; DB 1; Length 154; ; Pred. No. 2e-16; 29; Mismatches 52; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 >154 17 kDa SURFACE ANTIGEN.
20 20 N-ACYL DIGLYCERIDE (PROBAL
154 154 15967 MW; E3AA833346FAC320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 -----GOYCREYTOTVVIGGKOOKAYGNACROPDGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR 153
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01-OCT-1996 (Rel. 34, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
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154 AA
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37.8%;
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Best Local Similarity 37.00.
ما 59; Conservative
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STANDARD;
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N-ACYL DIGLYCERIDE (PROBABLE)

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STRAIN=Ohio 83-441;
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                                               SEQUENCE
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LIPID
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                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :::|:: | | :::||| | SKIMVIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL 63
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                       Pretzman C.I., Stothard D.R., Ralph D., Clark J.B., Fuerst P.A.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
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Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                       PROSTIE; PS00013; PROKAR, LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

SIGNAL 1 19 BY SIMILARITY.

20 154 17 Aba SURFACE ANTIGEN.

LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 31.1%; Score 259; DB 1; Length 154; Local Similarity 36.5%; Pred. No. 1.2e-15; les 57; Conservative 30; Mismatches 53; Indels
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154 AA; 15897 MW; SD06F45F9DBD5EEC CRC64;
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OLGUTE membrane; Lipoprotein; Antigen; Signal.
SIGNAL 1 9 SIMILARITY.
CHAIN 20 >-154 17 kDa SURFACE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 KOERROOYCREFOOKAMIAGOKOEIYGTACPOPDGR 153
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 kDa surface antigen precursor (Fragment)
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                                                                                                                                                                                                                                                                                                                                                          EMBL; U17008; AAA82040.1;
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                                                                                                 anchor (Probable).
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01-OCT-1996 (
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P50931;
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SEQUENCE
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                                                                                                                                                                                                                                                                                     GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                                                                                                                                                                                                                         64 GAVLGGQIGAGMDEQDRRLABLITSQRALETAPSGSNVEWRNPDNGNYGYITPNKTY---- 119
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64 GAVLGGQIGAGMDEQDRRLABLTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
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                                                                                                            Gaps
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Rickettsiaceae; Rickettsieae; Rickettsia.
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EMBL; U11017; AAB07705.1; -.

EMBL; U11017; AAB07705.1; -.

PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

Outer membrane; Lipoprotein; Antigen; Signal.

20 >154 17 kDa SURFACE ANTIGEN.

20 >154 17 kDa SURFACE ANTIGEN.

N-ACYL DIGLYCERIDE (PROBABLE)
                                                      Length 154;
                                                   31.1%; Score 259; DB 1; Length 154;
36.5%; Pred. No. 1.2e-15;
tive 30; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Indels
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154 AA; 15881 MW; A09C53B8769E31DA CRC64;
154 AA; 15895 MW; OCF85AD5D96DFEFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR 153
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                                                                                                                                                                                                                                                                                                                                                                                                          118 KOERROOYCREFOOKAMIAGOKOEIYGTACPOPDGR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 256; DB 1;
Pred. No. 2.2e-15;
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
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01-0CT-1996 (Rel. 34, Last annotation updat
17 kDa surface antigen precursor (Fragment)
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                                                                                                                  57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anchor (Probable).
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P50927 17KD RICAM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 GQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWR
                       Azad A.F., Sacci J.B. Jr., Nelson W.M., Dasch G.A., Schmidtmann E.T., Carl M.; "Genetic characterization and transovarial transmission of a typhus-like rickettsia found in cat fleas."; Proc. Natl. Acad. Sci. U.S.A. 89:43-46(1992).
-!- SUBCELIULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
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"A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine uptake in Escherichia coli.";
J. Bacteriol. 174:1029-1035(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 AA; 8372 MW; AD289A48EAB19E0E CRC64;
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InterPro; IPR000437; Prok lipoprot.
PROSITE; PS00013; PROKAR LIPOPROTEIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 37, Last annotation update)
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Pred. No. 4.8e-
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SEQUENCE FROM N.A.
STRAIN=ATCC 51872 / WA-C / Serotype 0:8;
MEDLINE=92121089; Pubmed=1732192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane lipoprotein pcp precursor
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   MEDLINE=92108069; PubMed=1729713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 NPDTGNSYSVEPVRTYQ 114
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(Rel. 26, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Conservative
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15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 SKIMIIALAASTLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C., Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=33989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U11013; AAB07704.1; -. EMBL; U11013; AAB07704.1; -. PROSITE; PS00013; PROKAR LIPORROTEIN; 1. OUTCHER membrane; Lipoprotein; Antigen; Signal. SIGNAL .. 19 BY SIMILARITY. 20 >154 17 kDa SURFACE ANTIGEN. N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.6%; Score 255; DB 1; Length 154; Best Local Similarity 36.5%; Pred. No. 2.6e-15; Matches 57; Conservative 29; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 KOERROOYCREFQOKAMIAGOKOEIYGTACPOPDGR 153
120 -RNSTGQYCREYTQTVVIGGKQQKAYGNACLQPDGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 AA
                                                                                                                                                                                                                                                                                                                        17 kDa surface antigen precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kDa surface antigen (Fragment)
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        Rickettsia amblyommii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MO 85-1084;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                             17KD RICAM
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RESULT 10 17KD\_RICCA ID 17KD\_RI AC P29697;

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SEQUENCE FROM N.A.
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Best Local S:
Matches 34
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AVAIDADYTIGGANNNTLSGDVFSASQAKQVQTVTYGTLLSVRPVTIQGGDDNNVMGAIG 66
                                                                                                                                                                                                                                                                                              -----VGAAT 33
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MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan B., Sun H., Florae L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES=S.typhimurium;
MEDLINE=96133688; PubMed=8544813;
Ludwig A., Tengel C., Bauer S., Bubert A., Benz R., Mollenkopf H.-J.,
Goebel W.;
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "SlyA, a regulatory protein from Salmonella typhimurium, induces haemolytic and pore-forming protein in Escherichia coli."; Mol. Gen. Genet. 249:474-486(1995).
                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                     DB 1; Length 155;
                                                                                                                                 (POTENTIAL).
                                                                                                         18 15 OUTER MEMBRANE LIPOPROTEIN PCP.
18 18 N-ACYL DIGLYCERIDE (POTENTIAL).
155 AA; 15362 MW; 8AD6BE2132E849FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     GAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                     13.5%; Score 112.5; DB 1; 24.7%; Pred. No. 0.0053; tive 19; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Last sequence update)
15-SFP-2003 (Rel. 42, Last annotation update)
10-SFP-2003 (Rel. 42, Last annotation update)
10-SFP-2003 (Rel. 42, Last annotation update)
11-SFP-2003 (Rel. 42, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --NOSLEKVKAGQVTRWRNPDTGNSYSVEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : :|: :| | 127 VQKQGPTRFSVGQ--RVMLASSGSTVTVSP 154
                                                                                                                                                                                                                                                                                              9 SLIIISVFLVGCAQN-----FSRQE----
                  PIR; S23787; S23787.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal.
                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 35, Created)
  EMBL; X60448; CAA42977.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhimurium, and Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:852-856(2001).
                                                                                                                                                                                                                          Best Local Similarity 24.7
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Q53549;
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                                                                                                                                                             SEQUENCE
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                                                                                              SIGNAL
                                                                                                                   CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 GOLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----IIISVFLVGCAQNFSRQEVGAATGAVVGGVA 41
                                                                                                                                  SPECIES-S.typhi...STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644564;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
J. Bacteriol. 185:2330-2337(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anchor (Potential).
-!- SIMILARITY: TO E.COLI SLYB, H.INFLUENZAE PCP AND Y.ENTEROCOLITICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                            J. Baccellular LOCATION: Attached to the outer membrane by a lipid
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.7%; Score 105.5; DB 1; Length 155; 24.3%; Pred. No. 0.021; Live 20; Mismatches 53; Indels 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 15 OUTER MEMBRANE LIPOPROTEIN 18 18 N-ACYL DIGLYCERIDE. 155 AA; 15548 MW; 82FDDCDCBABD55A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S80790; AABJJOJII.,
EMBL; AE008762; AAL20367.1; -.
EMBL; AL627271; CAD01922.1; -.
EMBL; AE016373; BLYB.
StyGene; SG10573; BLYB.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Complete proteome.
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Outer membrane lipoprotein slyB precursor.
SLYB OR B1641 OR Z2655 OR BCS2350 OR SF1668.
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MEDLINE=96133688; PubMed=8544813;
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NCBI_TaxID=562, 83334, 623;
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P55741; P76183;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Lart sequ
28-FEB-2003 (Rel. 41, Last ann
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Escherichia coli 0157:H7, and
Shigella flexneri.
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                                      enterica serovar Typhi CT:
Nature 413:848-852(2001).
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MBDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterohemorrhagic Escherichia coli Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
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-!- SUBCELLINIAR LOCATION: Attached to the outer membrane by a lipid anchor (Potential).
Ludwig A., Tengel C., Bauer S., Bubert A., Benz R., Mollenkopf H.-J.,
Goebel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.flexneri; STRAIN=301 / Serotype 2a; MEDLINE=22272406; PubMed=12384590; Jin W., Wang J., Liu H., Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                       SPECIES-E.coli; STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=E.coli; STRAIN=0157:H7 / BDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Garobeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                          "SlyA, a regulatory protein from Salmonella typhimurium, induces haemolytic and pore-forming protein in Escherichia coli."; Mol. Gen. Genet. 249:474-486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alba H., Baba T., Fullta K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Katiagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Mada C., Yamamoto Y., Horiuchi T.;

Yamamoto Y., Horiuchi T.;

A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
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                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12;
MEDLINE=97251357; Pubmed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:529-533(2001).
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MEDLINE-88115138; PubMed=2828309;
Delch R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;
"Cloning of genes encoding a 15,000-dalton peptidoglycan-associated
"Cloning of genes encoding an an antigenically related 15,000-dalton
protein from Haemophilus influenzae.";
J. Bacteriol. 170:489-498 (1988).
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STRAIN=Rd / KW20 / ATCC 51907;
MBDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last annotation update)
04.6F FBB-2003 (Rel. 41, Last annotation update)
04.7 Inter membrane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL cross-reacting lipoprotein).
PCP OR LPP OR HI1579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 104.5; DB 1; Length 155; Pred. No. 0.026;
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                                                                                       EMBL; D50807; BAA15402.1; --
EMBL; AB005387; AAG56630.1; --
EMBL; AB005258; BAB35773.1; --
EMBL; AB015187; AAN43250.1; --
EMBL; AB5771; B85771
PIR; C64921; C64921.
PIR; P590922; F90922; P60922; PROXAR LIPOPROTEIN; 1.
PROSITE; PS00013; PROXAR LIPOPROTEIN; 1.
PROSITE; PS00013; PROXAR LIPOPROTEIN; 1.
PROSITE; PS00013; PROXAR LIPOPROTEIN; 1.
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A -> T (IN REF. 2)
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                 entities requires a license agreement (@ or send an email to license@isb-sib.ch)
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                                                                          EMBL; AE000259; AAC74713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   12.6%;
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18
98
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  "Whole-genome random sequencing and assembly of Haemophilus influenzae
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MEDLINE=97061202; PubMed=890532;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ismoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
Ma 718-kb DNA sequence of the Escherichia coli K-12 genome
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SPECIES-E-COLI; STRAIN-KI2 / MG1655;
MEDLINE-97426617; Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                 -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 VGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.1%; Score 101; DB 1; Length 155; 39.6%; Pred. No. 0.052;
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"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Indels
                                                                                                             -!- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLYB AND TO Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; HI1579; -.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Complete proteome.
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NCBI_TaxID=562, 217992, 623;
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EMBL; U32832; AAC23228.1; -.
PIR; I64130; I64130.
                       Rd.";
Science 269:496-512(1995)
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Escherichia coli O6, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=E.coli; STRAIN=KI2;
MEDLINE=81236546; PubMed=6265208;
Young J.G., Rogers B.L., Campbell H.D., Jaworowski A., Shaw D.C.;
"Nucleotide sequence coding for the respiratory NADH dehydrogenase of
Escherichia coli. UNG initiation codon.";
Eur. J. Blochem. 116:165-170(1981).
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                                                                                                                                                                                                    MEDLINE=22388234; PubMed=12471157; Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Buckee D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang J., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 5 25 POTENTIAL.
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-!- SIMILARITY: TO RICKETTSIA 17 kDa SURFACE ANTIGEN.
                                                                                                                             SEQUENCE FROM N.A.
SPECIES=B.coli; STRAIN=06:H1 / CFT073 / ATCC 700928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      of uropathogenic Bscherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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EMBL; V00306; -; NOT ANNOTATED CDS.

EMBL; AE015138; AAN42732.1; ALT_INIT.

BTR; C64855; C64855.

EcoGene; EG12444; ycfJ.
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MEDLINE=95075659; PubMed=7984428;
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Search completed: November 5, 2003, 20:13:25 Job time : 6.39551 secs

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19agc7 rickettsia

Q8vue8 brucella ab

08/927 brucella me 09/2189 rhizobium m 09/2181 pseudomonas 02/8141 pseudomonas 02/8141 pseudomonas 02/8141 pseudomonas 02/818 and 02/218 and 02/218 and 02/218 and 02/218 ariante of 02/218 aria

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SUZYK M.A., Burian J., Thornton J.C., Kay W.W.;
"Identification of a genus-common Rickettsial surface antigen in the salmonid pathogen Piscirickettsia salmonis.";
Submitted (SEP-199) to the EMBL/GenBank/DDBJ databases.
SEMBL, AF184152; AAG17000.1; -.
SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64;
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Piscirickettsiaceae, Piscirickettsia.
NCBI_TaxID=1238;
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094K1U8
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09f9f2 rickettsia
05225 male-killin
09k2n6 male-killin
031065 rickettsia
09544W male-killin
05114 rickettsia
08k1t4 rickettsia
09f09 rickettsia
09f01 rickettsia
052637 rickettsia
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MEDLINE-1217364; PubMed=11321078;
BOUYET D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L.,
Zavala-Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
                                                                                                                                                                                                                                                                                                                                              Davis M.J., Ying Z., Brunner B.R., Pantoja A., Ferwerda F.H.;
"Rickettsial relative associated with papaya bunchy top disease.";
Curr. Microbiol. 36:80-84(1998).
EMBL; U76907; AAC02809.1; -.
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Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=42862;
                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=789;
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.Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
EMBL; AF195118; AAG28452.1; -
SEQUENCE 159 AA; 16497 MW; 34C5B020AF470A1F CRC64;
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                                                                                                                                  Last sequence update)
Last annotation update)
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Rickettsia felis (Rickettsia azadi).
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MEDLINE=98087556; Pubmed=9425244;
                                                                                                                                                                            17 kDa common-antigen (Fragment).
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79 --IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIA 136
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Billings A.N., Teltow G.J., Walker D.H.;

Molecular characterization of a novel spotted fever group rickettsial species from Ixodes scapularis in Texas.";

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AF031534; AAB95267.1; -.
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Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Schulenburg H.J.G.V.D., Majerus M.E.N.;
Bertrand D., Hurst G.D.D., Majerus M.E.N.;
"On the evolution of male-killing: Monophyletic origin and horizontal
rransfer of male-killing Rickettsia (a-Proteobacteria) from two con-
generic ladybirds, Adalia bipunctata L. and A. decempunctata L.
(Coleoptera: Coccinellidae) ";
Submitted (ARP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269518; CAB96383.1;
EMBL; AJ269517; CAB96382.1;
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| ::| :|| ||:||:
64 GAVLGGQIGAGMDEQDRRLAELITSQRALEATPSGTSVEWRNPDNGNHGYVTPNKTY
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male-killing Ricketteia from Adalia bipunctata.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Rickettsiaceae; Rickettsia.
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                                                                                                                              118 KOERROQYCRFFQQKAMIAGOKQEIYGTACPOPDGRWQVIS 158
                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
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Rickettsia cooleyi.
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80 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
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                                                                                                                       MEDLINE=20575219; PubMed=11133455;
Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Bertrand D., Hurst G.D.D., Majerus M.E.N.;
Incidence of male-killing Rickettsia spp. (alpha-Proteobacteria)
the Ten-Spot Ladybird Beetle Adalia decempunctata L. (Coleoptera:
Coccinellidae).";
                                                                                                                                                                                                                                                                                                                                                    30.2%; Score 251.5; DB 2; Length 144; 39.4%; Pred. No. 5.2e-15; ive 24; Mismatches 45; Indels 11;
 male-killing Rickettsia from Adalia decempunctata.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=120393;
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Baird R.W., Lloyd M., Stenos J., Ross B.C., Stewart R.S., Dwyselard R.W., Lloyd M., Stenos J., Ross B.C., Stewart R.S., Dwyselardzeterization and comparison of Australian human spotted; group rickettsiae.";

J. Clin. Microbiol. 30:2896-2902(1992).

EMBI. M99191, AAA73386.1;

SEQUENCE 154 AA; 15849 MW; F5C35855EDB439D2 CRC64;
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Rickettsiaceae, Rickettsieae, Rickettsia.
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35.3%; Pred. No. 2.7e-14;
ive 31; Mismatches 54;
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EMBL, AJ269516; CAB96381.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence
01-CT-2002 (TrEMBLrel. 22, Last annoctati
(Clone PRB FISF 1), S' end CDS (Fragment)
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17 kDa antigen (Fragment)
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                                                                                                           SEQUENCE FROM N.A
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MEDLINE=99045882; PubMed=9828442;

MEDLINE=99045882; PubMed=9828442;

Stenos J., Roux V., Walker D., Raoult D.;

Rickettsia honei sp. nov., the aetiological agent of Flinders Island spotted fever in Australia.";

Int. J. Syst. Bacteriol. 48:1399-1404(1998).

EMBL; AF027124; AAB81846.1; -.

EMBL; AF060706; AAD2033.1; -.
                                                                                                                                 25 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I
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                                     Length 144;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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Billings A.N., Yu X.-J., Teel P.D., Walker D.H.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
144 AA; 14785 MW; C8254739CCA56AE7 CRC64;
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Last annotation update)
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                                                                          24; Mismatches 45;
                                   30.3%; Score 252.5; DB 2 39.4%; Pred. No. 4.2e-15;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
17 kDa antigen (17 kDa protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                 137 AA
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                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                        52; Conservative
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                                                                                                                                                                                                                                                                140 QEIYGTACPQPD 151
                                                                                                                                                                                                                                                                                                 131 ÓKAÝGNÁCROPD 142
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                                 Query Match
Best Local Similarity
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Q9K4W8;
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80 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 GAVLGGQIVAGMDEQDRRLAELTSQRALEAAPSGSNVEWRNPDNGNYGYVTPNKTY--- 119
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                                                                                                                     10 NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGAGLLGAVLGGQJGAGMDEQDRRLAEL
                                                                                               25 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35789;
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01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
17 kDa protein (Fragment).
Rickettsia sp. California 2.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                   ch 29.0%; Score 241.5; DB 2; Length 1 1 Similarity 39.1%; Pred. No. 3.7e-14; 50; Conservative 24; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Nilsson K., Pahlson C.,
"Novel peptide diagnostic reagent and kit for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF181036; AAG09427.1; -.
NON_TER 151 151
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SEQUENCE 151 AA; 15621 MW; B77407B9C71E4B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Outer membrane protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 239; DB 2;
Pred. No. 7.3e-14;
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y 35.9%; Pred. No. /...
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                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                              140 QEIYGTAC 147
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STRAIN=California 2;
Raoult D.;
                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             Genchi C.;
"First detection of spotted fever group rickettsiae in Ixodes ricinus
"First detection of spotted fever group rickettsiae in Ixodes ricinus
Erom Italy.";
Emerg. Infect. Dis. 8:983-986(2002).
EMBL; AJ427883; CAD20879.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genchi C.; "First detection of spotted fever group rickettsiae in Ixodes ricinus
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STRAIN=17117A3;
MEDIJINE=221260; PubMed=12194779;
Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=IrITA2;
MEDLINE=22182650; PubMed=12194779;
Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiaae; Rickettsia.
NCBI_TaxID=184232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.0%; Score 241.5; DB 2; Length 131; 39.1%; Pred. No. 3.7e-14; Live 24; Mismatches 43; Indels 11
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=184231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 AA; 13358 MW; D4152713C9FAA9CA CRC64;
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                                                                                                                                 (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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23, Last annotation update)
124 GQD-----CRVYTQTVVIGGKQQKAYGNACRQPDGQ 154
                                                                                               131 AA
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01-0CT-2002 (TrEMBLrel. 22, Last seg
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Emerg. Infect. Dis. 8:983-986(2002)
EMBL; AJ427882; CAD20878.1;
                                                                                               PRT;
                                                                                                                                                                                       membrane protein (Fragment).
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                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
Genchi C.;
"First detection of spotted fever group rickettsiae in Ixodes ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simser J.A., Palmer A.T., Munderloh U.G., Kurtti T.J.;
"Isolation of a spotted fever group rickettsia, Rickettsia peacockii, in a Rocky Mountain wood tick, Dermacentor andersoni, cell line."; Appl. Environ. Microbiol. 67:546-552(2001).

EMBL; AF260571; AAF69012.1; -.
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=47589;
                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
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Local Similarity 38.3%; Pred. No. 1.3e-13;
nes 49; Conservative 24; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AA; 13383 MW; D78C171050CAA9CA CRC64;
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                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
17 KDa surface antigen (Fragment).
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   131 AA
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Emerg. Infect. Dis. 8:983-986(2002)
EMBL; AJ427881; CAD20877.1; -...
   PRT;
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MEDLINE=22182650; PubMed=12194779;
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MEDLINE=21091941; PubMed=11157215;
   PRELIMINARY;
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Q9L522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGAGALLGAVLGGQIGAGMDEQDRRLAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK---I 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I
                                                                                                                                                                                                                                                                                                                                                                                                                 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                      Query Match 28.4%; Score 236.5; DB 2; Length 131; Best Local Similarity 38.3%; Pred. No. 1e-13; Matches 49; Conservative 24; Mismatches 44; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsia sp.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=789;
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"A new SFG rickettsia isolated from fleas.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                SEQUENCE FROM N.A.
STRAIN=California 2;
Roux V., Raoult D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210693; AAG48554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 AA; 13344 MW; AIDCF71050DF52DF CRC64;
                                                                                                                                                                                                                                                                                                  13374 MW; 23C8819B29FFF860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
17 kDa antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AA
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J. Bacteriol. 176:388-394(1994).
EMBL; U04162; AAA19235.1; -.
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RESULT 13 Q52637

DDT ACCOUNT THE SECTION OF SECTIO

Gaps

11;

DB 2; Length 131;

th 28.3%; Score 235.5; DB 2; Length 131; Similarity 38.3%; Pred. No. 1.3e-13; 49; Conservative 24; Mismatches 44; Indels 11.

> 14 RESULT Q8KLU2

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Db 10 NKQCTGTLLGGAGGALLGSQFGKGQL-VGVGYGALLGAVLGGQIGAGMDEQDRRLAEL 68

Qy 80 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRITYGRYNKQERRQQYCREFQQKAMIAGGK 139

Db . 69 TSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY-----RNSTGQYCREYTQTVVIGGKQ 123

Qy 140 QEIYGTAC 147

Db 124 QKAYGNAC 131

Search completed: November 5, 2003, 20:15:04
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Fora, 974 Page

Ford, V.

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Seg. 105 2, 4

Sequence 22817, A Sequence 19701, A Sequence 19701, A Sequence 4769, Ap Sequence 4769, Ap Sequence 85693, Ap Sequence 16, Appl

Appli Appli Appli Appli

equence 169, App Sequence 169, App Sequence 22817, A

Sequence 169, Sequence 4 Sequence 6 Sequence 6 Sequence 6

3827, Ap 3827, Ap 3363, Ap 10773, A

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

319, App 27, Appl

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

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Sequence 2, Application US/09677374

Sequence 2, Application US/09677374

GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Ruzyk, Michael
APPLICANT: Thornton, Julian
APPLICANT: Trace of INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDC01/60485/US
CURRENT APPLICATION NUMBER: US/09/677,374
CURRENT FILING DATE: 2000-09-15
PRIOR PLILNG DATE: 2000-09-15
PRIOR PLILNG DATE: 2000-09-15
PRIOR PLILNG DATE: 2000-09-18
PRIOR PLILNG DATE: 2000-09-18
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PRIOR PLILNG DATE: 2000-09-18
PRIOR PLILNG DATE: 2000-09-18
PRIOR PLILNG DATE: 2000-09-18
PRIOR PLILNG DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
ALIGNMENTS
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128.5
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101.5
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1068.647 Million cell updates/sec
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                                                                                                                                     November 5, 2003, 20:12:57; Search time 137.938 Seconds
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1 MNRGCLQGSSLIIISVFLVG......IYGTACRQFDGRWQVISTEK 162
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1: /cgn2_6/ptodata/1/paa/BCTUS COMB.pep:*

2: /cgn2_6/ptodata/1/paa/USO6_COMB.pep:*

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18: /cgn2_6/ptodata/1/paa/USO93_COMB.pep:*

19: /cgn2_6/ptodata/1/paa/USO93_COMB.pep:*

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10: /cgn2_6/ptodata/1/paa/USO9_COMB.pep:*

                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                 5728757 seqs, 909918778 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Score

Result 8

Post-processing:

Database :

Scoring table:

Searched:

Perfect score:

Sequence:

OM protein

Run on:

Sequence 5127

Sequence 7664

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APPLICANT: Kay, William
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETISIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDCO1/60485/US
CURRENT FILING DATE: 2000-09-15
FRIOR PPLICATION NUMBER: US 60/154,437
PRIOR PPLICATION NUMBER: US 60/154,437
PRIOR PPLICATION NUMBER: US 60/154,437
PRIOR PPLICATION NUMBER: US 2000-09-15
PRIOR PPLICATION NUMBER: E 2000/0752
PRIOR PPLICATION NUMBER: E 2000/0752
PRIOR PPLICATION NUMBER: E 2000-09-18
PRIOR PPLICATION NUMBER: CL 2544-2000
PRIOR PPLICATION NUMBER: CL 2544-2000
PRIOR PPLICATION NUMBER: CL 2544-2000
PRIOR PLING DATE: 2000-09-18
PRIOR PPLICATION NUMBER: CL 2544-2000
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PRECEIT VEFFICE OF SEQ ID NOS: 20
SOFTWARE: PRECEIT VEFFICE OF SEQ ID NOS: 20
SOFTWARE: PRECEIT VEFFICE OF SEQ ID NOS: 20
SEQ ID NOS: 20
SEQ ID NOS: 20
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APPLICANT: Kuzyk, Michael A.
APPLICANT: Kuzyk, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Kay, William V.
APPLICANT: Torntcon, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
FRIOR APPLICATION NUMBER: US 69/677,374
FRIOR PILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE PATENTING VERSION 3.0
SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
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Pred. No. 7.8e-81;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 815; DB 20;
Pred. No. 7.8e-81;
1; Mismatches 1;
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ORGANISM: Piscirickettsia salmonis
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Best Local Similarity 98.8%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 98.8
Matches 158; Conservative
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APPLICANT: Burian, Jan
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Julian C.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VECKTISIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT PILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 99/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VETSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ERROGYCREFQOKAMIAGOKOEIYGTACROPDGRWOVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ERRÓGYCKEFGGKAMIAGGKGEIYGTACRÓPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 836; DB 28;
Best Local Similarity 100.0%; Pred. No. 3.8e-83;
Matches 162; Conservative 0; Mismatches 0;
                                                                                                                                                                                        Query Match
100.0%; Score 836; DB 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-83;
Matches 162; Conservative 0; Mismatches 0;
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                                                                                                    ; ORGANISM: Piscirickettsia salmonis
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GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Kuzyk, Michael
APPLICANT: Thornton, Julian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/10261446; GENERAL INFORMATION:
                  SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162
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LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: University of Iowa Research Foundation, Inc., et al.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
TITLE OF INVENTION: BIOFILM FORMATION
CURRENT APPLICATION NUMBER: PCT/US02/12532
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 815; DB 28;
Pred. No. 1.5e-80;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169
LENGTH: 182
                              PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US02-12532-169; Sequence 169, Application PC/TUS0212532; GENERAL INFORMATION:
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; APPLICANT: Whiteley, Marvin
                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Piscirickettsia salmonis
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PCT-US02-12532-169
   2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.5%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SIGNAL
LOCATION: (-95)..(-1)
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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US-10-127-032-169
                                                                                                                                                                                                                                                        LENGTH: 256
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Sequence 6, Application US/09677374

GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Kuzyk, Wichael
APPLICANT: Thornton, Julian
APPLICANT: Troncon, Julian
APPLICANT: TANDERTON: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDCO1/60485/US
CURRENT APPLICATION NUMBER: US/09/677,374
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: NO 2004637
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
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APPLICANT: Kay, William W.
APPLICANT: Thornton, Juliam C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 46.16-64.094
CURRENT APPLICATION NUMBER: US/10/261,446
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                                        GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                         62 GGLIGSKIGOSMDQODKIKLNOSLEKVKAGOVTRWRNPDIGNSYSVEPVRTYQRYNKOER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                 123 ROOYCREFOOKAMIAGOKOBIYGTACROPDGRWOVISTEK 162
                                                                                                                                                                                                  123 ROQYCREFQOKAMIAGOKOEIYGTACROPDGRWOVISTEK 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Piscirickettsia salmonis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SIGNAL
LOCATION: (-95)..(-1)
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US-09-677-374-6
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APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH03-04
CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 09/252,991
     INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 ÓLAGTÁIGÁVVGGLLGNQIGGGTGKKIATVAGÁVGGGYAGNKVQEGMQERDTYTTETRC 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 15.4%; Score 128.5; DB 30; I Similarity 34.8%; Pred. No. 4e-05; 32; Conservative 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.9%; Score 116; DB 29; 25.0%; Pred. No. 0.00078; tive 21; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 -KLNQSLEKV-----KAGQVTRWRNP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 STVHDSSEKVVGYDVKYMLDGKAGOIRMERDP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNRGCLQGSSLIIISVFLVGC----AQNFSRQE-
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AND TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
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132 STRAYVQQVDQGQIFR 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rubenfield, Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.04
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 32; Conserv
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US-10-366-683-19701
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                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
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APPLICANT: Deloughery, Craig
APPLICANT: Deloughery, Craig
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATHOJ - 04
CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT APPLICATION NUMBER: 09/252,991
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22817
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        APPLICANT: Bangera, M. Gita
APPLICANT: Lory, Stephen
APPLICANT: Lory, Stephen
APPLICANT: Greenberg, Everett Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
TITLE OF INVENTION: BIOFILM FORMATION
TITLE OF INVENTION: BIOFILM FORMATION
CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR PILING DATE: 2001-024
NUMBER OF SEQ ID NOS: 170
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 27; Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.4%; Score 128.5; DB 27; Best Local Similarity 34.8%; Pred. No. 3.7e-05; Matches 32; Conservative 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 -KLNQSLEKV------KAGQVTRWRNP 100
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; Sequence 22817, Application US/10419128
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT CRGANISM: Pseudomonas aeruginosa US-10-127-032-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas aeruginosa
US-10-366-683-22817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-366-683-22817
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Sequence 4769. Application US/10603114
GENERAL INFORMATION:
APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILL TITLE OF INVENTION: US/10/603,114
CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT PILING DATE: 2003-06-24
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 TIGGGTGRNLATAAGAIAGGAAGQAQGALNTTKGVQLEVRLDSGKTVVVVQKADNTAYR 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 114.5; DB 31; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 GAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.00
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 85693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 85693, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STR.
TITLE OF INVENTION: METHODS OF USE THERE
FILE REFERENCE: 261/210
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| | CQRVAVIGNGNNLTVSP 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.4%;
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 25.4
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GCLQGSSL-----
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US-09-791-537-85693
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US-09-791-537-85693
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT PAPLICATION NUMBER: US/09/543,681A
CURRENT PAPLICATION NUMBER: US/09/543,681A
PRIOR APPLICATION NUMBER: US/09/04-05
PRIOR PILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
APPLICANT: MAKE J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE PERERRYCE: 107196.136

CURRENT APPLICATION NUMBER: US/10/419,128

CURRENT APPLICATION NUMBER: US/09/252,991

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 19701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          ch 13.9%; Score 116; DB 30; Length 165; 1 Similarity 25.0%; Pred. No. 0.00078; 34; Conservative 21; Mismatches 41; Indels 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 114.5; DB 19;
; Pred. No. 0.0011;
19; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNRGCLQGSSLIIISVFLVGC----AQNFSRQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 QGQRVAVIGNGNNLTVSP 165
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 STRAYVQQVDQGQIFR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.7%;
25.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.4
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GCLQGSSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-543-681A-4769
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Search completed: November 5, 2003, 20:25:12 Job time : 138.938 secs

us-09-677-374-2.rapm

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 5, 2003, 20:13:32 ; Search time 9.23316 Seconds (without alignments) 824.821 Million cell updates/sec Run on:

US-09-677-374-2 836

1 MNRGCLQGSSLIIISVFLVG.....IYGTACRQPDGRWQVISTEK 162 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

248976 seqs, 47010500 residues Searched:

248976

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending Patents AA New:\*

(cgn2\_6/ptodata/2/paa/PCT NEW COMB.pep:\*

(cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*

(cgn2\_6/ptodata/2/paa/US07 NEW COMB.pep:\*

(cgn2\_6/ptodata/2/paa/US08 NEW COMB.pep:\*

(cgn2\_6/ptodata/2/paa/US08 NEW COMB.pep:\*

(cgn2\_6/ptodata/2/paa/US08 NEW COMB.pep:\*

(cgn2\_6/ptodata/2/paa/US08 NEW COMB.pep:\*

(cgn2\_6/ptodata/2/paa/US08 NEW COMB.pep:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result<br>No. | Score | %<br>Query<br>Match | %<br>Query<br>Match Length | DB | ID                   | Description       |
|---------------|-------|---------------------|----------------------------|----|----------------------|-------------------|
| 7             | 836   | 100.0               | 162                        | 9  | US-10-241-602B-6     | Sequence 6, Appli |
| 7             | 836   | 100.0               | 162                        | 9  | US-10-261-445B-2     | 7                 |
| m             | 815   | 97.5                | 161                        | 9  | US-10-261-445B-4     | 4                 |
| 4             | 815   | 97.5                | 256                        | 9  | US-10-261-445B-6     | 9                 |
| 2             | 112   | 13.4                | 20                         | 9  | US-10-261-445B-16    | 16,               |
| 9             | 105.5 | 12.6                | 223                        | Ŋ  | US-09-581-286A-434   | 434               |
| 7             | 105.5 | 12.6                | 230                        | 'n | US-09-581-286A-309   | 30                |
| œ             | 97.5  | .11.7               | 106                        | ഹ  | US-09-897-516A-5133  |                   |
| 6             | 83.5  | 10.0                | 66                         | 9  | US-10-389-647-605    |                   |
| 10            | 81.5  | 9.7                 | 734                        | 9  | US-10-425-114A-49440 |                   |
| 11            | 80    | 9.6                 | 403                        | S  | US-09-897-516A-7766  | Sequence 7766, Ap |
|               | 80    | 9.6                 | 515                        | 9  | US-10-679-063-22745  |                   |
| 13            | 80    | 9.6                 | 517                        | 9  | US-10-679-063-22744  | Sequence 22744, A |
| 14            | 80    | 9.6                 | 1755                       | Н  | PCT-US03-26780-3444  | Sequence 3444, Ap |
| 15            | 80    | 9.6                 | 2599                       | Ŋ  | US-09-674-546A-1669  | Sequence 1669, Ap |
| 16            | 79    | 9.4                 | 593                        | 9  | US-10-435-696-50     | Sequence 50, Appl |
| 17            | 79    | 9.4                 | 1261                       | 9  | US-10-679-063-16542  |                   |
| 18            | 92    | 9.1                 | 293                        | Н  | PCT-US03-28227-2863  | Sequence 2863, Ap |
| 19            | 9/    | 9.1                 | 423                        | ч  | PCT/US02/39429-8     |                   |
| 20            | 74    | 8.9                 | 800                        | 9  | US-10-296-115-1229   | 12                |
| 21            | 74    | 8.9                 | 820                        | н  | PCT-US03-28227-5403  | uı                |
| 22            | 74    | 8.9                 | 871                        | Н  | PCT-US03-31442-3     |                   |
| 23            | 73.5  | 8.8                 | 390                        | Н  | PCT-US02-38594-98    | 98                |
| 24            | 73.5  | 80.00               | 390                        | ٦  | PCT-US02-38594-100   | 100,              |
| 25            | 73.5  | 8.8                 | 404                        | Н  | PCT-US02-38594-96    | 96, 7             |
| 26            | 73.5  | 8.8                 | 404                        | 7  | US-60-487-610-2773   | 2773              |

| Sequence 4, Appli<br>Sequence 70833, A   |                   | Sequence 2711, Ap   | Sequence 24, Appl | Sequence 71, Appl | Sequence 7, Appli | Sequence 40, Appl | Sequence 5, Appli | Sequence 38, Appl | Sequence 1796, Ap  | Sequence 932, App | Sequence 3, Appli | Sequence 6, Appli | Sequence 4405, Ap   | Sequence 14, Appl | Sequence 22287, A   | Sequence 2783, Ap  | Sequence 1525, Ap  |
|--|-------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|---------------------|-------------------|---------------------|--------------------|--------------------|
| US-09-743-818A-4<br>US-10-425-114A-70833 | PCT-US03-10856A-5 | PCT-US03-26780-2711 | US-10-689-006-24  | US-09-743-818A-71 | US-09-743-818A-7  | PCT-US02-24483-40 | US-09-743-818A-5  | PCT-US02-24483-38 | US-60-487-610-1796 | US-10-472-928-932 | PCT-US03-32968-3  | PCT-US03-32968-6  | US-09-897-516A-4405 | US-08-592-070D-14 | US-10-679-063-22287 | US-60-487-610-2783 | US-60-487-610-1525 |
| s v                                      | Н                 | Н                   | 9                 | വ                 | Ŋ                 | н                 | Ŋ                 |                   | 7                  | 9                 | Н                 | Н                 | Ŋ                   | 4                 | 9                   | 7                  | 7                  |
| 733                                      | 254               | 2322                | 261               | 515               | 571               | 692               | 698               | 711               | 757                | 89                | 101               | 101               | 399                 | 405               | 512                 | 541                | 563                |
| 8.8                                      | 8.7               | 8.7                 | 8.7               | 8.7               | 8.7               | 8.7               | 8.7               | 8.7               | 8.7                | 8.6               | 8.6               | 8.6               | 8.6                 | 9.8               | 8.6                 | 9.8                | 9.8                |
| 73.5                                     | 73                | 73                  | 72.5              | 72.5              | 72.5              | 72.5              | 72.5              | 72.5              | 72.5               | 72                | 72                | 72                | 72                  | 72                | 72                  | 72                 | 72                 |
| 27                                       | 29                | 30                  | 31                | 32                | 33                | 34                | 35                | 36                | 37                 | 38                | 39                | 40                | 41                  | 42                | 43                  | 44                 | 45                 |

## ALIGNMENTS

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61 VLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
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0
                                                                                                                    APPLICANT: STRUMEN, MALIALIE
APPLICANT: BURGALG, MALIALIE
APPLICANT: Jones, Simon
APPLICANT: Jones, Simon
APPLICANT: Gones, Simon
APPLICANT: Gones, Simon
APPLICANT: Walenzuela, Pablo
APPLICANT: Burzio, Luis
TITLE OF INVENTION: Sequences from Piscirickettsia salmonis
FILE REFERENCE: H-32319A
CURRENT APPLICATION NUMBER: US/10/241,602B
CURRENT FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: PCT/GB01/01055
PRIOR APPLICATION NUMBER: GB0005838.8
PRIOR APPLICATION NUMBER: GB0016080.4
PRIOR APPLICATION NUMBER: GB0016080.4
PRIOR FILING DATE: 2000-07-01
PRIOR PILING DATE: 2000-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 836; DB 6;
100.0%; Pred. No. 6.4e-65;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
                                             Sequence 6, Application US/10241602B
GENERAL INFORMATION:
APPLICANT: Simard, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 162, Conservative
RESULT 1
US-10-241-602B-6
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APPLICANT: Kuzyk, Michael A.
APPLICANT: Kuzyk, Michael A.
APPLICANT: Kuzyk, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Ray, William W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64095
CURRENT APPLICATION NUMBER: US/10/261,445B
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MISTA, MISTAN, ALGRED A.
APPLICANT: MISTAN, MISTAN A.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
CURRENT PLICATION NUMBER: US/10/261,445B
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR PRILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
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                                                                                                                              62 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
2 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
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                                                                                                                                                                                                                                                          122 RÓGYCREFŐGKAMIAGÓKÖEIYGTÁCPOPDGRWOVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
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Pred. No. 7.1e-63;
1; Mismatches 1.
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GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10261445B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

Best Local Similarity 98.8%;
Matches 158; Conservative
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; LOCATION: (-95)..(-1)
US-10-261-445B-6
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                                                                                                                 APPLICANT: RUZYK, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64095
CURRENT APPLICATION NUMBER: US/10/261,445B
CURRENT FILING DATE: 2002-09-15
PRIOR PAPLICATION NUMBER: US 60/577,374
PRIOR FILING DATE: 1999-09-17
NUMBER: US 60/154,437
NUMBER: PATENTING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Thornton, Julian W.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
CURRENT APPLICATION NUMBER: US/10/261,445B
CURRENT FILING DATE: 2000-09-15
PRIOR PPLICATION NUMBER: US 60/677,374
PRIOR PPLICATION NUMBER: US 60/154,437
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VARIED NOS: 20
SOFTWARE: PATENTIN VARIED NOS: 20
SOFTWARE: PATENTIN VARIED NOS: 20
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SOFTWARE: PATENTIN VARIED NOS: 20
SOFTWARE: PATENTIN VARIED NOS: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 836; DB 6;
100.0%; Pred. No. 6.4e-65;
rative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10261445B
GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
                                                               Sequence 2, Application US/10261445B GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 162; Conservative
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US-10-261-445B-4
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NUMBER OF SEQ ID NOS: 20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
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PRIOR APPLICATION NUMBER: PCT/AU98/01023
PRIOR PILING DATE: 1999-12-10
PRIOR PLILNG DATE: 1997-12-10
PRIOR PLILNG DATE: 1997-12-10
PRIOR PLILNG DATE: 1997-12-10
PRIOR PLILNG DATE: 1997-12-31
PRIOR FILING DATE: 1999-01-10
PRIOR PLILNG DATE: 1999-01-10
PRIOR PLILNG DATE: 1998-01-10
PRIOR PLILNG DATE: 1998-01-10
PRIOR PLILNG DATE: 1998-01-10
PRIOR PLILNG DATE: 1998-03-10
PRIOR PLILNG DATE: 1998-03-10
PRIOR PLILNG DATE: 1998-04-09
PRIOR PLILNG DATE: 1998-04-09
PRIOR PLILNG DATE: 1998-04-03
PRIOR PLILNG DATE: 1998-05-05
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-05
PRIOR PLING DATE: 1998-07-07
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                                                                                                                                                                                                        Query Match
13.4%; Score 112; DB 6; L
Best Local Similarity 100.0%; Pred. No. 0.00095;
Matches 20; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 434, Application US/09581286A
GENERAL INFORMATION:
APPLICANT: ROSS, BRUCE C.
APPLICANT: BARR, IAN G.
APPLICANT: AGIUS, CATHERINE T.
APPLICANT: ROTHEL, INDA J.
APPLICANT: ROTHEL, INDA J.
APPLICANT: MARGETTS, MAL B.
APPLICANT: WORKING, DIANNA M.
APPLICANT: WEBB, ELIZABETH A.
                                                                                     ; TYPE: PRT
; ORGANISM: Piscirickettsia salmonis
US-10-261-4458-16
                                                                                                                                                                                                                                                                                                                            110 PVRTYQRYNKQERRQQYCRE 129
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SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 20
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Best Local Similarity 36.1%
Matches 26; Conservative
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66 ALIGKKWDKOKK 77
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APPLICANT: ROTHEL, LINDA 1.
APPLICANT: ROTHEL, LINDA 1.
APPLICANT: ROTHEL, LINDA 1.
APPLICANT: ROTHEL, LINDA 1.
APPLICANT: HOCKING, DIANNA M.
TILLE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
FILE REPRENCE: 4137-3.
FILE REPRENCE: 4137-3.
FILE REPRENCE: 1998-12-10
PRIOR PELLING DATE: 1998-12-10
PRIOR PELLING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: AU PP 182
PRIOR PILING DATE: 1997-12-31
PRIOR PELLING DATE: 1998-01-30
PRIOR PELLING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR PELLING DATE: 1998-01-30
PRIOR FILING DATE: 1998-03-10
PRIOR PELLING DATE: 1998-03-10
PRIOR PELLOR NUMBER: AU PP 2264
PRIOR PELLING DATE: 1998-04-05
PRIOR PELLING DATE: 1998-04-05
PRIOR PELLING DATE: 1998-04-05
PRIOR PELLING DATE: 1998-05-05
PRIOR PELLING DATE: 1998-05-02
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TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 721
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Slater, Steven C.
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Sequence 309, Application US/09581286A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Porphyromonas gingivalis
US-09-581-286A-309
                                                              APPLICANT: ROSS, BRUCE C.
APPLICANT: BARR, IAN G.
APPLICANT: PATTERSON, MICHELLE A.
APPLICANT: AGIUS, CATHERINE T.
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Best Local Similarity 36.13
These 26; Conservative
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73 ALIGKKMDKQKK 84
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US-09-897-516A-5133
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Gaps

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137 VIADGNGVTEGQEDHCLKNETVNNVVA------NADEGNSGAVECFQTYKRKHAKSSS 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Stater, Steven C.
APPLICANT: Spiridonov, Serven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Kenchabdus sp. Genome Sequences And Uses Thereof FILE, REFERENCE: 38-21(51847) B
CURRENT APPLICATION NUMBER: US/09/897,516A
                                                                                                                                                                                                                                                                                                                                         29;
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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
                                                                                                                                                                                                                                                                                          Length 734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 403;
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                                                                                                                                                                                                                                                                                          DB 6;
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9.6%; Score 80; DB 5;
Best Local Similarity 34.2%; Pred. No. 19;
Matches 26; Conservative 11; Mismatches 3:
                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: 700991377_FLI.pep
US-10-425-114A-49440
                                                                                                                                                                                                                                                                                       Query Match 9.7%; Score 81.5; D
Best Local Similarity 25.5%; Pred. No. 29;
Matches 35; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        26 SRQEVGAATGAVVGGVA--GQLFGKGSGRV---
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7766, Application US/09897516A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-679-063-22745; Sequence 22745, Application US/10679063; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 QY-CREFQQKAMIAGQK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 EFKVQENSRKHMGAASQ 206
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                                                                                                                                             TYPE: PRT
ORGANISM: Glycine max
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven K.
APPLICANT: Tabaska, Jack B.
APPLICANT: Tabaska, Jack B.
APPLICANT: Tabaska, Jack B.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                         5
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                                                                                                                                                                                                                                                                                  Score 97.5; DB 5; Length 106;
Pred. No. 0.12;
8; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.0%; Score 83.5; DB 6; Length 99;
Best Local Similarity 32.9%; Pred. No. 1.8;
Matches 23; Conservative 9; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCOMMENTATION:

APPLICANT: GREENERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389, 647
CURRENT APPLICATION NUMBER: 09/653730
FRIOR APPLICATION NUMBER: 09/653730
FRIOR APPLICATION NUMBER: 60/153022
FRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 710
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 605
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                   28 QEVGAATGAVVGGVAGQLFGKGS--GRVAMAIGGAVLGGLIGSKI--
                      CURRENT APPLICATION NUMBER: US/09/897,516A CURRENT FILING DATE: 2001-06-29 PRIOR APPLICATION NUMBER: US 60/215,161 PRIOR FILING DATE: 2000-06-30 NUMBER OF SEQ ID NOS: 8415 LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49440, Application US/10425114A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 605, Application US/10389647 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 KTKIYTSTQVGRTCQFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 KIKLNQSLEKVKAGQVT 95
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 36.4%;
Matches 28; Conservative
FILE REFERENCE: 38-21 (51847) B
                                                                                                                                                                                                                  ORGANISM: Xenorhabdus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 -GAVLGGLIG 67
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61 MGAIAGGTVG 70
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80; DB 1;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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TWDYRDYGARNPQTYNDPKLFEEYRQ 2484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/674,546A CURRENT FILING DATE: 1999-04-30 NUMBER OF SEQ ID NOS: 3264 SOFTWARE: Patentin version 3.2 SEQ ID NO 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: November 5, 2003, 20:25:58 Job time: 10.2332 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 ------RTYQRYNKQERRQQYCRE 129
                   PRIOR APPLICATION NUMBER: 60/406,640
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR PILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,666
PRIOR APPLICATION NUMBER: 60/406,666
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1669, Application US/09674546A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.6%;
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.2 SEQ ID NO 3444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 43.99
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 19.34
Matches 40; Conservative
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PCT-US03-26780-3444
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APPLICANT'S FIVERPRIME THERAPEUTICS, INC.
APPLICANT'S FIVERPRIME THERAPEUTICS, INC.
APPLICANT'S FIVERPRIME THERAPEUTICS, INC.
TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLECTIDES AND METHODS OF TILE OF INVENTION: THEIR USE
FILE REFERENCE: 08940.0014-00304
CURRENT APPLICATION NUMBER: 60/406,616
PRIOR PILING DATE: 2002-08-29
PRIOR PILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,655
                                                                                                                                                                                                                                                                                                                                                                                                                 45 VAGNLHEGGMKKVVAARRPVLGELGNKVLRNASQDLLGKGVEKGAALKNANPTLKNIKPR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 VAGQLFGKGSGRVAMA-----IGGAVLGGLIGSKIGQSMDQQDKIK-LNQSLEKVKAG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 VAGQLFGKGSGRVAMA-----IGGAVLGGLIGSKIGQSMDQQDKIK-LNQSLEKVKAG 92
                                                                                                                                                                                                                                                                                                                                          8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)B
CURRENT PAPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
RIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 22744
                                                                                                                                                                                                                                                                                 ; Score 80; DB 6; Length 515;
; Pred. No. 25;
15; Mismatches 41; Indels
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25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 QVTRWRNPDTGNSYSVEPVRTYQRYNKQE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 OVTRWRNPDIGNSYSVEPVRTYORYNKOE 121
FILE REFERENCE: 38-15 (52054)B
CURRENT APPLICATION NUMBER: US/10/679, 063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415, 758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 22745
LENGTH: 515
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                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Anopheles gambiae str. PEST
US-10-679-063-22745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-10-679-063-22744
; Sequence 22744, Application US/10679063
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Anopheles gambiae str. PEST
US-10-679-063-22744
                                                                                                                                                                                                                                                                                        9.6%;
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Best Local Similarity 28.1%
Matches 75; Conservative
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Matches 25; Conservative
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APPLICANT: Chiron Corporation
TITLE OF INVENTION: Neisseria Meningitidis Antigens and Compositions
FILE REFERENCE: CHIR-0334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 SSLIIISVFLVGCAQNFSRQEV-----GAATGAVVGGVAGQLFGKG
                                                                                                                                                                                                                                                                                                                                                                                                            9.6%; Score 80; DB 5; Length 2599;
19.3%; Pred. No. 1.7e+02;
tive 32; Mismatches 45; Indels
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RESULT 1
US-09-677-374-4
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   November 5, 2003, 20:12:57; Search time 137.086 Seconds (without alignments) 1068.647 Million cell updates/sec
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1 MRGCLQGSSLIIISVFLVGC......IYGTACPQPDGRWQVISTEK
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1: /cgn2_6/ptodata/1/paa/US06_COMB.pep: *

2: /cgn2_6/ptodata/1/paa/US06_COMB.pep: *

4: /cgn2_6/ptodata/1/paa/US06_COMB.pep: *

5: /cgn2_6/ptodata/1/paa/US081_COMB.pep: *

6: /cgn2_6/ptodata/1/paa/US081_COMB.pep: *

7: /cgn2_6/ptodata/1/paa/US081_COMB.pep: *

6: /cgn2_6/ptodata/1/paa/US082_COMB.pep: *

7: /cgn2_6/ptodata/1/paa/US083_COMB.pep: *

9: /cgn2_6/ptodata/1/paa/US086_COMB.pep: *

10: /cgn2_6/ptodata/1/paa/US086_COMB.pep: *

11: /cgn2_6/ptodata/1/paa/US086_COMB.pep: *

12: /cgn2_6/ptodata/1/paa/US086_COMB.pep: *

13: /cgn2_6/ptodata/1/paa/US086_COMB.pep: *

14: /cgn2_6/ptodata/1/paa/US086_COMB.pep: *

15: /cgn2_6/ptodata/1/paa/US086_COMB.pep: *

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17: /cgn2_6/ptodata/1/paa/US091_COMB.pep: *

18: /cgn2_6/ptodata/1/paa/US091_COMB.pep: *

19: /cgn2_6/ptodata/1/paa/US091_COMB.pep: *

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10: /cgn2_6/ptodata/1/paa/US094_COMB.pep: *

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10: /cgn2_6/ptodata/1/paa/US094_COMB.pep: *

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12: /cgn2_6/ptodata/1/paa/US097_COMB.pep: *

13: /cgn2_6/ptodata/1/paa/US097_COMB.pep: *

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/cgn2_6/ptodata/1/paa/US100_COMB.pep:*
/cgn2_6/ptodata/1/paa/US10_COMB.pep:*
/cgn2_6/ptodata/1/paa/US102_COMB.pep:*
/cgn2_6/ptodata/1/paa/US103_COMB.pep:*
/cgn2_6/ptodata/1/paa/US103_COMB.pep:*
/cgn2_6/ptodata/1/paa/US103_COMB.pep:*
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prodata/1/paa/US099B_COMB.pep:*
                                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence 4, Appli

161 20 US-09-677-374-4

100.0

Score 832

Query Match Length DB

Result No.

Description

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APPLICANT: Burian, Jan
APPLICANT: Ruzyk, Michael
APPLICANT: Kuzyk, Michael
APPLICANT: Kuzyk, Michael
APPLICANT: Kay, Wiliam
APPLICANT: Ray, William
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION NUMBER: US/09/677,374
CURRENT FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 20
                                Sequence 6, Appli
Sequence 2, Appli
Sequence 169, Appli
Sequence 169, App
Sequence 22817, A
Sequence 27817, A
Sequence 4769, Ap
Sequence 4769, Ap
Sequence 16, Appl
Sequence 16, Appl
Sequence 19701, A
Sequence 19701, A
Sequence 2, Appli
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0 US-09-677-374-6

0 US-09-677-374-6

0 US-09-677-374-2

0 US-09-677-374-2

1 US-10-261-446-2

1 US-10-261-446-2

1 US-10-127-169

1 US-10-128-22817

1 US-10-128-22817

1 US-10-136-683-19701

1 US-10-136-683-19701

1 US-10-136-683-19701

1 US-10-18-561-4

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TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDCOJ/60485/US
CURRENT APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR PLING DATE: 2000-09-15
PRIOR PLING DATE: 2000-09-15
PRIOR PLING DATE: 2000-09-15
PRIOR PLING DATE: 2000-09-16
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PPLICATION NUMBER: UE 2000-09-18
PRIOR PPLICATION NUMBER: CL 2544-2000
PRIOR PLING DATE: 2000-09-18
PRIOR PPLING DATE: 2000-09-15
PRIOR PPLING DATE: 2000-09-15
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APPLICANT: Burian, Jan
APPLICANT: Ray, William W
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
CURRENT PAPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
PRIOR FILING DATE: 2002-09-15
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
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ORGANISM: Piscirickettsia salmonis
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ORGANISM: Piscirickettsia salmonis
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SOFWWARE: PatentIn version 3.0
SEQ ID NO ELEMENTH: 256
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LOCATION: (-95)..(-1)
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; LOCATION: (-95)..(-1)
US-09-677-374-6
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APPLICANT: Ray, William W.
APPLICANT: Thornton, Julian W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERRENCE: 4616-46094
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR PLING DATE: 2000-09-15
PRIOR PLING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOUTH AND APPLICATION NUMBER: US 60/154,437
NUMBER OF SEQ ID NOS: 20
SOUTH AND APPLICATION NUMBER OF SEQ ID NOS: 20
SEQ ID NO 4
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                                                                                                                                                                                                                                 Length 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
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                                                                                                                                                                                                                             Query Match 100.0%; Score 832; DB 20; Best Local Similarity 100.0%; Pred. No. 4.4e-83; Matches 161; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 832; DB 28;
Best Local Similarity 100.0%; Pred. No. 4.4e-83;
Matches 161; Conservative 0; Mismatches 0;
                                                                                                 TYPE: PRT
ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Piscirickettsia salmonis
US-10-261-446-4
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; Sequence 6, Application US/09677374
; GENERAL INFORMATION:
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Burian, Jan
APPLICANT: Kuzyk, Michael
APPLICANT: Thornton, Julian
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RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
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FILE REPERENCE: U12-O70CPPC
CURRENT APPLICATION NUMBER: PCT/US02/12532
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR PILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 170
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.0%; Score 815; DB 28; 98.8%; Pred. No. 3.4e-81; ative 1; Mismatches 1;
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                                     FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR PRIOR DATE: 1099-09-17
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US02-12532-169; Sequence 169, Application PC/TUS0212532; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
; ORGANISM: Piscirickettsia salmonis
US-10-261-446-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
PCT-US02-12532-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.8
Matches 158; Conservative
               TITLE OF INVENTION:
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US-10-127-032-169
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US-09-677-374-2

I Sequence 2, Application US/09677374

Sequence 2, Application US/09677374

Sequence 2, Application US/09677374

Sequence 2, Application US/09677374

Sequence 2, Application US/09677374

APPLICANT: Burian, Jan

APPLICANT: Kuzyk, Milliam

APPLICANT: Thornton, Julian

APPLICANT: Thornton, Julian

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST

TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY

FILE REPERENCE: 1DC01/60485/US

CURRENT APPLICATION NUMBER: US/09/677,374

CURRENT APPLICATION NUMBER: US 60/154,437

PRIOR APPLICATION NUMBER: US 2000-09-15

PRIOR PELING DATE: 2000-09-18

PRIOR PELING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: E 2000/0752

PRIOR APPLICATION NUMBER: CL 2544-2000

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kazy, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
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                                                                                                       1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
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                                              0; Gaps
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                                           Indels
                                                                                                                                                                                                                                                                                                                                                                             216 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
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            Pred. No. 8.3e-83;
100.0%; Pred. No.
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Best Local Similarity 98.8*
Matches 158; Conservative
                                        Matches 161; Conservative
            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-677-374-2
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Sequence 4769, Application US/09543681A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION:
DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
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GENERALDA INFORMATION:
A PROFILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.138
CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT APPLICATION NUMBER: US/09/252,991
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 OIAGTAIGAVVGGLLGNQIGGGTGKKIATVAGAVGGGYAGNKVOEGMOERDTYTTTETRC 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
15.3%; Score 127.5; DB 30;
Best Local Similarity 34.8%; Pred. No. 4.8e-05;
Matches 32; Conservative 13; Mismatches 28; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 WRNPD-----TGNSYSVEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 YRQGQRVAVIGNGNNLTVSP 165
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa US-10-419-128-22817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRGCLQGSSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Proteus mirabilis
US-09-543-681A-4769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Conservative
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Best Local Similarity
Matches 35; Conserv
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US-09-543-681A-4769
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US-10-603-114-4769
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GENERAL INFORMATION:
APPLICANT: Rubenifield, Marc J.
APPLICANT: Rubenifield, Marc J.
APPLICANT: Bosh, David
APPLICANT: Bush, David
APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH03-04
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR FILING DATE: 1999-02-18
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     APPLICANT: Bangera, M. Gita
APPLICANT: Lory, Stephen
APPLICANT: Lory, Stephen
TITLE GENERAT: Greenberg, Everett Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
TITLE OF INVENTION: BIOFILM FORMATION
FILE REFERENCE: UIZ-070CP
CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-02-4
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 169
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APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 34.8%
Matches 32, Conservative
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US-10-419-128-22817
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1.ENGTH: 192
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Sequence 16, Application US/10261446
; Sequence 16, Application US/10261446
; GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
; APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISBASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION RICKETTSIAL DISBASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION WUMBER: US/10/261,446
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR PILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENTING DATE: DALENTION OF SEQ ID NOS: 20
SEQ ID NO 16
SEQ ID NO 16
                       APPLICANT: KLZYK, Michael
APPLICANT: KLZYK, Michael
APPLICANT: KLZYK, Michael
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
APPLICANT: TAY, WIlliam
APPLICANT: KAY, WILLiam
TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDCO1/60485/US
CURRENT APPLICATION NUMBER: US 60/154,437
PRIOR PLILING DATE: 2000-09-15
PRIOR PLILING DATE: 2000-09-18
PRIOR PLILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
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100.0%; Pred. No. 0.00011;
ive 0; Mismatches 0;
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Job time : 137.086 secs
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ORGANISM: Piscirickettsia salmonis
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Best Local Similarity 100.C
Matches 20; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AVALAAVTLIGCANNNTLSGDVFSASQAKQVQTVTYGTLLSVRPVTIQGGDDNNVMCAIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 GOLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEK-----VKAGQVTR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRGCLQGSSL-------IIISVFLVGCAQNFSRQEVGAATGAVVGGVA
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Best Local Similarity 24.7%; Pred. No. 0.0016;
Matches 37; Conservative 19; Mismatches 43; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 31; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 GAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL-
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%; Score 114.5; DB 3
25.0%; Pred. No. 0.0011;-
:ive 20; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 --NOSLEKVKAGQVTRWRNPDTGNSYSVEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 VOKOGPTRFSVGQ--RVMLASSGSTVTVSP 154
                               FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
FRIOR APPLICATION NUMBER: US/09/543,681
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 SLIIISVFLVGCAQN-----FSRQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-677-374-16; Sequence 16, Application US/09677374; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 WRNPD-----TGNSYSVEP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Yersinia enterocolitica
US-09-791-537-85693
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 25.09
Matches 35, Conservative
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-603-114-4769
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 5, 2003, 20:13:32; Search time 9.17617 Seconds (without alignments) 824.821 Million cell updates/sec Run on:

US-09-677-374-4 Perfect score: Title:

832 1 MRGCLQGSSLIIISVFLVGC......IYGTACPQPDGRWQVISTEK 161 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

248976 segs, 47010500 residues Searched:

248976 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/2/paa/USO6\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/paa/USO6\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/paa/USO7\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/paa/USO9\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/USO9\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/USO9\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/2/paa/USO9\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/2/paa/USO9\_NEW\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|   | Description    |   | Sequence 4, Appli | ý                | Sequence 6, Appli | 7                | 16,               | 434,               | Sequence 309, App  | Sequence 5133, Ap   | 605, 7            | 8, A             | 4944                 | Sequence 114, App  | 20,              |                     |                  |                     |                   |                     | Seguence 22744, A   | Sequence 3444, Ap   | Sequence 1669, Ap   | Sequence 5, Appli | equence 2863, Ap    | Sequence 1229, Ap  | Sequence 5403, Ap   | 'n               |
|---|----------------|---|-------------------|------------------|-------------------|------------------|-------------------|--------------------|--------------------|---------------------|-------------------|------------------|----------------------|--------------------|------------------|---------------------|------------------|---------------------|-------------------|---------------------|---------------------|---------------------|---------------------|-------------------|---------------------|--------------------|---------------------|------------------|
|   | De             |   | ű                 | Š                | ŭ                 | Š                | Š                 | ŭ                  | Š                  | Š                   | ഗ്                | ű                | ഗ്                   | ഗ്                 | Š                | Š                   | Š                | ഗ്                  | ά                 | Š                   | Š                   | Š                   | Š                   | Š                 | Š                   | Š                  | ű                   | Š                |
|   | ID             |   | US-10-261-445B-4  | US-10-261-445B-6 | US-10-241-602B-6  | US-10-261-445B-2 | US-10-261-445B-16 | US-09-581-286A-434 | US-09-581-286A-309 | US-09-897-516A-5133 | US-10-389-647-605 | PCT/US02/39429-8 | US-10-425-114A-49440 | PCT-US03-21510-114 | US-10-435-696-50 | US-10-679-063-16542 | US-10-689-006-24 | US-09-897-516A-7766 | PCT-US02-39429-88 | US-10-679-063-22745 | US-10-679-063-22744 | PCT-US03-26780-3444 | US-09-674-546A-1669 | PCT-US03-10856A-5 | PCT-US03-28227-2863 | US-10-296-115-1229 | PCT-US03-28227-5403 | PCT-US03-31442-3 |
|   | DB             | į | ø                 | ø                | 9                 | 9                | 9                 | S                  | Ŋ                  | S                   | 9                 | ٦                | 9                    | ٦                  | φ                | 9                   | 9                | ß                   | Н                 | 9                   | 9                   | Н                   | 'n                  | -                 | -1                  | 9                  | ٦                   | -                |
|   | Length         |   | 191               | 256              | 162               | 162              | 20                | 223                | 230                | 106                 | 66                | 423              | 734                  | 1117               | 593              | 1261                | 261              | 403                 | 438               | 515                 | 517                 | 1755                | 2599                | 254               | 293                 | 800                | 820                 | 871              |
| ф | Query<br>Match |   | 100.0             | 100.0            | 98.0              | 98.0             | 13.5              | 12.3               | 12.3               | .11.4               | 10.4              | 10.0             | o.<br>0              | 9.6                | 9.5              | 9.5                 | 9.4              | 9.4                 | 9.4               | 9.4                 | 9.4                 | 9.3                 | 9.3                 | 8.8               | 8.8                 | 8.8                | 8.8                 | 8.8              |
|   | Score          |   | 832               | 832              | 815               | 815              | 112               | 102.5              | 102.5              | 94.5                | 86.5              | 83               | 82.5                 | 79.5               | 79               | 79                  | 78.5             | 78                  | 78                | 78                  | 78                  | 77                  | 77                  | 73                | 73                  | 73                 | 73                  | 73               |
|   | Result<br>No.  |   | -                 | 7                | m                 | 4                | 2                 | 9                  | 7                  | 80                  | 6                 | 10               | 11                   | 12                 | 13               | 14                  | 15               | 16                  | 17                | 18                  | 19                  | 20                  | 21                  | 22                | 23                  | 24                 | 25                  | 26               |

Sequence 6, Application US/10261445B; GENERAL INFORMATION:
APPLICANT: Krzyk, Michael A.
SAPLICANT: Burian, Jan
APPLICANT: Kay, William W.

RESULT 2 US-10-261-445B-6

| Sequence 2711, Ap Sequence 19, Appl Sequence 1712, Ap Sequence 64061, A Sequence 52050, A Sequence 118, Appl Sequence 59401, A Sequence 189, Appl Sequence 4797, Appl Sequence 4797, Appl Sequence 2779, Appl | Sequence 932, App<br>Sequence 43688, A<br>Sequence 72589, A<br>Sequence 20, Appl      |
|---|---|
| PCT-US03-26780-2711 US-10-435-614-19 US-10-679-663-7732 US-10-425-114A-54061 US-10-425-114A-54061 US-10-418-861B-77 US-10-425-114A-59401 US-00-830-321A-3 US-09-976-858-128 PCT-US03-128234-38 PCT-US03-18234-38 PCT-US03-18234-39 PCT-US03-28227-4797  | US-10-472-928-932<br>US-10-425-114A-43688<br>US-10-425-114A-72589<br>US-10-435-614-20 |
| 1151556766661   | φφφφ  |
| 2322<br>2602<br>3488<br>4299<br>10646<br>1811<br>3115<br>456<br>690<br>733<br>738   | 224<br>230<br>260   |
| $\begin{smallmatrix} \alpha & \alpha & \alpha & \alpha & \alpha & \alpha & \alpha & \alpha & \alpha & \alpha $  | 8 8 8 8<br>7 5 5 5  |
| 73<br>72.5<br>72.5<br>72.7<br>72.7<br>71.5<br>71.5<br>71.5<br>71.5<br>71.5  | 71 71 71 71   |
| 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2   | 4 4 4 4<br>5 6 4 3  |

# ALIGNMENTS

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APPLICANT: BALTIAN, MINITED TO THE APPLICANT: BALTIAN, MINITED TO THE APPLICANT: BALTIAN, Jan APPLICANT: Thornton, Julian C.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY CURRENT APPLICATION NUMBER: US/10/261,445B
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 199-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 832; DB 6;
100.0%; Pred. No. 3.2e-66;
ive 0; Mismatches 0;
                     Sequence 4, Application US/10261445B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 161, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-261-445B-4
US-10-261-445B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
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1; Mismatches
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GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/10261445B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.8%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-10-261-445B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-261-445B-2
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## APPLICANT: Thornton, Julian C.

TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST

TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY

FILE REPERENCE: 4616-64095

CURRENT PELICATION NUMBER: US/10/261,445B

CURRENT PELING DATE: 2002-09-30

FRIOR APPLICATION NUMBER: US 60/154,437

PRIOR APPLICATION NUMBER: US 60/154,437

PRIOR PILING DATE: 1999-09-17

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PACENTIN Version 3.0

SOFTWARE: PACENTIN Version 3.0

SOFTWARE: 256

TYPE: PRI

ORGANISM: Piscirickettsia salmonis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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### APPLICANT: STOWNERS, Houb
### APPLICANT: Brouwers, Houb
#### APPLICANT: Globe, Simon
### APPLICANT: Globe, Simon
### APPLICANT: Globe, Simon
### APPLICANT: Globe, Dais
### APPLICANT: Burzio, Luis
### APPLICANT: Burzio, Luis
### APPLICANT: Burzio, Luis
### REPERENCE: H-3319A
### CURRENT APPLICATION NUMBER: US/10/241,602B
### CURRENT APPLICATION NUMBER: C002-09-11
### PRIOR PILING DATE: 2001-03-12
### PRIOR PILING DATE: 2000-03-11
### PRIOR PILING DATE: 2000-03-11
### PRIOR PILING DATE: 2000-03-11
### PRIOR PILING DATE: 2000-07-01
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GENERAL INFORMATION:
APPLICANT: Simard, Nathalie
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Best Local Similarity 98.8
Matches 158; Conservative
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; LOCATION: (-95)..(-1)
US-10-261-445B-6
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APPLICANT: Burian APPLICANT: Ray, William W.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Unlian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY FILE REFERENCE: 4616-64095
CURRENT APPLICATION NUMBER: US/10/261,445B
CURRENT FILING DATE: 2002-09-30
PRIOR FILING DATE: 2002-09-15
PRIOR FILING DATE: 2002-09-15
PRIOR FILING DATE: 1999-09-17
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APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: UALIAN C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH ACAINST
TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-641095
CURRENT FILING DATE: 2002-09-30
PRIOR PILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 1999-09-17
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                                                                                     GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                               62 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
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2 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
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Pred. No. 1e-64;
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                                                                                                                                                                                                                                                                        123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTBK 162
                                                                                                                                                                                                                        122 RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
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Sequence 309, Application US/09581286A GENERAL INFORMATION:
                                                                                                                                                                                                  APPLICANT: ROSS, BRUCE C.
APPLICANT: BARR, IAN G.
APPLICANT: PATTERSON, MICHELLE
APPLICANT: AGIUS, CATHERINE T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-897-516A-5133
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APPLICANT: ROSS, BRUCE C.
APPLICANT: BARRY ING G.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: MARCHELLE A.
APPLICANT: MARCHELLE INDA J.
APPLICANT: MARCHELLE B.
APPLICANT: MARCHEL, BLANKA M.
APPLICANT: WEBB, ELIZABETH A.
APPLICANT: WEBB, ELIZABETH A.
APPLICANT: WEBB, ELIZABETH A.
APPLICANT: WINDER: US/09/501,206A
CURRENT APPLICATION: DATE: 2000-06-28
FILE REPRENCE: 1397-12-10
FRIOR APPLICATION NUMBER: AU PP 0839
FRIOR FILING DATE: 1997-12-10
FRIOR FILING DATE: 1997-12-31
FRIOR FILING DATE: 1998-01-30
FRIOR FILING DATE: 1998-01-30
FRIOR PELING DATE: 1998-01-30
FRIOR PELING DATE: 1998-04-03
FRIOR FILING DATE: 1
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                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                   0; Indels
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13.5%; Score 112; DB 6; I
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 20; Conservative 0; Mismatches 0;
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ORGANISM: Porphyromonas gingivalis
                                                                                                                                   ; TYPE: PRT
; ORGANISM: Piscirickettsia salmonis
US-10-261-445B-16
                                                                                                                                                                                                                                                                                                                                                                                                                   109 PVRTYQRYNKQERRQQYCRE 128
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
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                                                               SEQ ID NO 16
LENGTH: 20
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APPLICANT: ROTHEL, LINDA J.
APPLICANT: ROTHEL, LINDA J.
APPLICANT: MARGETTS, MAL B.
APPLICANT: MARGETTS, MAL B.
APPLICANT: WERBER, DIANNA M.
APPLICANT: WEBB. ELIZABETH A.
ITILE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
FILE REPERBENCE: 4137-3
CURRENT APPLICATION NUMBER: US/09/581,286A
CURRENT APPLICATION NUMBER: US/09/581,286A
CURRENT FILING DATE: 1998-12-10
PRIOR FILING DATE: 1997-12-10
PRIOR FILING DATE: 1997-12-31
PRIOR PLING DATE: 1997-12-31
PRIOR PLING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-04-23
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PRIOR FILING DATE: 1998-05-22
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PRIOR FILING DATE: 1998-05-22
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PRIOR FILING DATE: 1998-05-22
PRIOR PLING DATE: 1998-05-22
PRIOR PLING DATE: 1998-07-22
PRIOR PLING DATE: 1998-05-22
PRIOR PLING DATE: 1998-07-22
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GENERAL INFORMATION:
APPLICANT: Corbin, Dair R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Krasomil-Osterfeld, Karina C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Porphyromonas gingivalis US-09-581-286A-309
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Spiridonov, Serge
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Best Local Similarity 34.7*
Matches 25, Conservative
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LENGTH: 423
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                                                                                                                                                                                                                          Score 94.5; DB 5; Length 106;
Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GREENERG, E. Peter
APPLICANT: GREENERG, Martin
APPLICANT: GCHUSTER, Martin
APPLICANT: LOSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REPRENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                 27 QEVGAATGAVVGGVAGQLFGKGS--GRVSMAIGGAVLGGLIGSKI----
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                               9; Mismatches
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
SEQ ID NO 5133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NeoRx Corporation
APPLICANT: Goshorn, Stephen Charles
APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Lin, Yukang
APPLICANT: Lin, Yukang
APPLICANT: Reno, John M.
APPLICANT: Beno, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-389-647-605; Sequence 605, Application US/10389647; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application PC/TUS0239429 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                         78 KIKLNOSLEKVKAGOVT 94
                                                                                                                                                                                                                                                                                                                                                                                                          krkivrsroverrcorr 80
                                                                                                                                                                                                                         Query Match
Best Local Similarity 35.1%;
Matches 27; Conservative
                                                                                                                                                  TYPE: PRT
ORGANISM: Xenorhabdus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 -GAVLGGLIG 66
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61 MGAIAGGTVG 70
                                                                                                                                                                                      US-09-897-516A-5133
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FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- genc
PCT/US02/39429-8
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Soreen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
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APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Norderic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 GSGGGGGGGGGG---GGGSSDIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 -----SLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREF--QQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 GSSPKFWIYATSNIASGVPARFSGSGSGTSYSL----TISRVBABDAATYYCQQWISNPP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 -----GOSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 GAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 SRQEVGAATGAVVGGVA--GQLFGKGSGRVS------MAIGGAVLG---GLIGSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 83; DB 1; Length 423;
Pred. No. 8.7;
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REPERRNCE: 690022.54701PC CURRENT APPLICATION NUMBER: PCT/US02/39429 CURRENT FILING DATE: 2002-12-06 WUMBER OF SEQ ID NOS: 92 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      10.0%; Scor.
21.7%; Pred. No. 8..,
... 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 TFGAGTKLELKSSGSGSADPSKDSKAQVSAAE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 AMIAGQKQEI----YGTACPQPDGRWQVISTE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: 700991377_FLI.pep
US-10-425-114A-49440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
9.9%; Score 82.5; Di
Best Local Similarity 25.5%; Pred. No. 19; '
Matches 35; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 QY-CREFQQKAMIAGQK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 EFKVQENSRKHMGAASQ 206
                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 21.7%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Glycine max
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US-10-425-114A-49440
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Sequence 24, Application US/10689006
GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Vanderbilt University
APPLICANT: Marnaugh Raymond
TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
FILE REFERENCE: 1242/72
CURRENT FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: US/10/689,006
CURRENT FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
PRIOR PILING DATE: 2001-08-30
PRIOR PLING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
                                               66 GSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 ------SQEDHIRIRTKWHPVLAGELDAWR------LSLNPAQ--QAYLQEKKRISY 301
-GRVSMAIGGAVLGGLIGSKIGQSMDQQ 76
                                                                                                                              ----GQVTRWRNPDTGNSYSVEPVRTYQRYNK 118
                                                                                                                                                                                        146 EKVTMONLNDRLASYLDKVRALEESNYELEGKIKEWYEKH-GNSHOGEP-RDYSKYYK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 GAATGAVVG------GVAGQLFGKGSG-----RVSMAIGG-----AVLGGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
TILE REFERENCE: 38-15(52054)B
CURRENT APPLICATION NUMBER: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 16542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 79; DB 6; Length 1261; 24.8%; Pred. No. 73; tive 17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Indels
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US-10-689-006-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.4%; Score 78.5; 19.3%; Pred. No. 12;
   23 NFSROEVGAATGAVVGG--VAGQLFGKGS
                                                                                                                                                                                                                                                                                                                             US-10-679-063-16542
; Sequence 16542, Application US/10679063
; GENERAL INFORMATION:
                                                                                                                              77 DKI-----KLNQSLEKVKA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Magnetococcus sp. MC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.8%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 19.3%
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 C 126
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US-10-689-006-24
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LENGTH: 261
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                 Sequence 114, Application PC/TUS0321510

GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: MP21S AS MODIFIERS OF THE D21 PATHWAY AND METHODS OF USE
FILE REFERENCE: EXO3-046C-PC
CURRENT APPLICATION NUMBER: PCT/US03/21510
CURRENT PILING DATE: 2003-07-09
PRIOR FILING DATE: 2003-07-09
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/411,010
PRIOR PILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-18-07
PRIOR FILING DATE: 2002-18-05-16
PRIOR FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PATCHTIN VERSION 3.2
SEQ ID NO 114
LENGTH: 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 QOQPTVNTSRFRVVKLDSSSEPFKKGRWTCTEFYEKENAVPATEGVLINKVVETVKQNPI 500
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GENERAL INFORMATION:
APPLICANT: Wirter, Ralph
APPLICANT: Winnes, Marc
APPLICANT: Winnes, Marc
APPLICANT: Winnes, Marc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSI
TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
FILE REPERENCE: LeA 36 108
CURRENT APPLICATION NUMBER: US/10/435,696
CURRENT PILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: EP02003112.4
PRIOR APPLICATION NUMBER: EP02010291.9
PRIOR PILING DATE: 2003-05-01
NUMBER OF SEQ ID NOS: 314
SOFTWARE: PALENTING DATE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.6%; Score 79.5; DB 1; I Best Local Similarity 21.2%; Pred. No. 57; Matches 41; Conservative 25; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 DK-----IKLNQSLEKVKAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 QVTRWRNPDTGNSYSVEPVRTYQRYNK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 QKQEI-YGTACPQ 149
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560 TLQQMDFGSTGPQ 572
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US-10-435-696-50
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   PCT-US03-21510-114
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US-10-435-696-50
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Search completed: November 5, 2003, 20:25:58 Job time : 9.17617 secs

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APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
TITLE OF INVENTION: VACCITES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: IDCO1/60485/US
CURRENT APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: NO 20004637
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR PLILING DATE: 2000-09-16
PRIOR FILING DATE: 2000-09-18
PRIOR PRILING DATE: 2000-09-18
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PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 20
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Sequence 9, Appli
Sequence 12, Appli
Sequence 12, Appl
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Sequence 65163, A
Sequence 19761, A
Sequence 124659,
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Sequence 2, Appli
Sequence 4, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 8, Appli
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US-09-677-374-4

US-10-261-446-4

US-10-261-446-2

US-10-261-446-2

US-10-261-446-2

ECT-US00-00708-10

PCT-US00-00708-10

PCT-US00-00708-10

PCT-US00-00708-10

US-09-808-898-22

US-09-808-898-22

US-08-965-888-2

US-08-96-59-968-2

US-08-965-98-2

US-09-91-537-19761

US-09-791-537-19664

US-09-791-537-14534

US-09-791-537-1483

US-09-791-537-1483

US-09-791-537-1483

US-09-791-537-1483

US-09-791-537-1888-4

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GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Kuzyk, Michael
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188.5
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                                                                                      November 5, 2003, 20:12:57; Search time 217:976 Seconds (without alignments) 1068.647 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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6661, Ap 51483, A 17654, A 10882, A 74713, A 30993, A 84844, A

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APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Kuzyk, Michael
APPLICANT: Thornton, Julian
APPLICANT: Thornton, Julian
APPLICANT: Transcon, Julian
APPLICANT: Kay, William
ITILE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPRENCE: IDCO1/60485/US
CURRENT FILING DATE: 2000-09-15
PRIOR PELICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: ED 2000/0752
PRIOR APPLICATION NUMBER: ED 2000/0752
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
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APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
                                                                                                                                                                                               156 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
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61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
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Best Local Similarity 100.0%; Pred. No. 2.4e-78;
Matches 161; Conservative 0; Mismatches 0;
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, APPLICANT: Kuzyk, Michael A.
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APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: TACATOR, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 69/677,374
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR PILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
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100.0%; Score 1335; DB 28; Length 256;
Best Local Similarity 100.0%; Pred. No. 7.1e-131;
Matches 256; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                            ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 6, Application US/10261446; GENERAL INFORMATION: ; APPLICANT: Kuzyk, Michael A.
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  SOFTWARE: PatentIn version 3.0
                                                                                                                                   ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (-95)..(-1)
US-09-677-374-6
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LOCATION: (-95).
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LENGTH: 256
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LENGTH: 256
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APPLICANT: BLIAD, Jan
APPLICANT: BLIAD, Jan
APPLICANT: Tornton, Julian W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
CURRENT APPLICATION NUMBER: US/10/261,446
PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
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63 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
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GENERAL INFORMATION:
APPLICANT: Levy, Ilan
APPLICANT: Shoseyov, Oded
APPLICANT: Nosseyov, Oded
TITLE OF INVENTION: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
FILE REFERENCE: 00/20910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                              217 RQQYCREFQQXAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 ROOYCREFOOKAMIAGOKQEIYGTACPOPDGRWQVISTEK 256
                                                                                                                            123 RÓGYCREFGGKAMIAGGKGEIYGTACROPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 815; DB 28;
Pred. No. 1.5e-76;
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Best Local Similarity 46.8%; Pred. No. 5.2e-42;
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CURRENT FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 13
SOTTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10261446
GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
APPLICANT: Burian, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.8%;
Matches 158; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 162
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| Sequence 2, Application US/09677374
| Sequence 2, Application US/09677374
| GENERAL INFORMATION:
| APPLICANT: Burian, Jan
| APPLICANT: Kay, William
| APPLICANT: Kay, William
| TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY AGAINST
| TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
| FILE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
| FILE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
| FILE OF INVENTION: WIMBER: US/09/677,374
| CURRENT APPLICATION NUMBER: US 60/154,437
| PRIOR APPLICATION NUMBER: IE 2000/09-15
| PRIOR PILING DATE: 2000-09-15
| PRIOR APPLICATION NUMBER: EB 000-09-18
| PRIOR PILING DATE: 2000-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV 155
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Pred. No. 1.5e-76;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
62.3%; Score 832; DB 28;
Best Local Similarity 100.0%; Pred. No. 2.4e-78;
Matches 161; Conservative 0; Mismatches 0;
                        CURRENT APPLICATION NUMBER: US/10/261,446
CURRENT FILING DATE: 2002-09-30
FRIOR APPLICATION NUMBER: US 09/677,374
FRIOR APPLICATION NUMBER: US 60/154,437
FRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Piscirickettsia salmonis
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ORGANISM: Piscirickettsia salmonis
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Best Local Similarity 98.8%;
Matches 158; Conservative
   FILE REFERENCE: 4616-64094
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                                                                                                                      121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                        -----KKĞQFITIQ------ 111
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                                                                                                                                                                                                                         ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP------KVTGYIGGAK--VL 153
APPLICANT: Levy , llan
APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Shoseyov, Oded
APPLICANT: Nussinovitch, Amos
TITLE OF INVENSINOVITCH: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
FILE REFERENCE: 00/20910
CURRENT APPLICATION NUMBER: PCT/US00/00708
CURRENT PILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID WO 10
LENGTH: 326
TYPE: PRT
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                                                                        61 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE---------------
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LOCATION: (30)..(208)
OTHER INFORMATION: taken from Clostridium cellulovorans
NAME/KEY: misc_feature
LOCATION: (226)..(326)
                                                                                                                                                        --------FGFASGRATL-----
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OTHER INFORMATION: taken from bovine
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PCT-US00-00708-10
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PCT-US00~00708-6
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LGNSYVDNTSKYTANFVKETASPISTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
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Sequence 6, Application PC/TUS0000708

GENERAL INFORMATION:
APPLICANT: Levy, ilan
APPLICANT: Shoseyov, Oded
APPLICANT: Nussinovitch, Amos
APPLICANT: Nussinovitch, Amos
APPLICANT: Nussinovitch, Amos
PITLE OF INVENTION: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
FILE REFERENCE: 00/20910
CURRENT APPLICATION NUMBER: PCT/US00/00708
CURRENT FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Levy, ilan
APPLICANT: Shoseyov, Oded
APPLICANT: Nussinovitch, Amos
TITLE OF INVENTION: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
FILE REPERENCE: 00/20910
CURRENT APPLICATION NUMBER: PCT/US00/00708
CURRENT FILING DATE: 2000-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSVEFYNSNKSAQTHSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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Pred. No. 1.1e-41;
9; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
36.5%; Score 487; DB 1;
Best Local Similarity 46.8%; Pred. No. 1.2e-41;
Matches 116; Conservative 12; -Mismatches 30;
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                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; Clostridium cellulovorans PCT-US00-00708-6
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SOFWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 163
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Best Local Similarity 51.7%;
Matches 106; Conservative
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61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCL---QGSSLIIISVFLVGCAQ 117
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APPLICANT: Yosef, Karmey
APPLICANT: Shpiegl, Itai
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, ROY H.
TITLE OF INVENTION: METHODS OF DETECTION USING THE
TITLE OF INVENTION: CELLULOSE BINDING DOWAIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
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SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
CIP OF PCT/US94/04132
FILING DATE:
APPLICATION NUMBER:
CIP OF PCT/US94/04132
ATTORNEY/AGENT INFORMATION:
NAME:
NAME:
NAME:
REFERENCE/DOCKET NUMBER:
TOWNEY/AGENT INFORMATION:
NAME:
REFERENCE/DOCKET NUMBER:
TOWNEY/AGENT INFORMATION:
NAME:
REFERENCE/DOCKET NUMBER:
TOWNEY/ATTORNEY/AGENT INFORMATION:
NAME:
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; Pred. No. 7e-41;
10; Mismatches 33;
                            PRIOR FILING DATE: 1996-11-25
PRIOR APPLICATION NUMBER: 08/597,274
PRIOR FILING DATE: 1996-02-06
PRIOR APPLICATION NUMBER: 08/908,909
PRIOR FILING DATE: 1997-08-08
PRIOR PILING DATE: 1997-08
PRIOR PILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESS:
STREET: 1155 AVENUE OF THE AMERICAS
TITY: NEW YORK
TATE: NEW YORK
TATE: NEW YORK
TATE: NEW YORK
TATE: 1036
1 1036
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   APPLICATION NUMBER: 08/757,046
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US-08-330-394-2
Sequence 2, Application US/08330394
GENERAL INFORMATION:
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62.6%;
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(212) 869-8864
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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US-09-808-898-22
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Best Local Simil
Matches 107; C
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GENERAL INFORMATION:
Sequence 22, Application US/0980898
GENERAL INFORMATION:
Bryan, Bruza
APPLICANT: Stant-Gyorgyi, Christopher
APPLICANT: Szczepaniak, William
TITLE OF INVENTION: RENILLA RENIFORNESCENT PROTEINS, NUCLEIC ACIDS ENCODING TITLE OF INVENTION: ELOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH TH
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REPERBNOE: 24729-128
CURRENT APPLICATION NUMBER: US/09/808,898
CURRENT FILING DATE: 2001-03-15
PRIOR PILING DATE: 2000-03-15
PRIOR FILING DATE: 1999-03-26
121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application PC/TUS0000708
GENERAL INFORMATION:
APPLICANT: Levy, 11an
APPLICANT: Shoseyov, Oded
APPLICANT: Nussinovitch, Amos
TITLE OF INVENTION: MODIFICATION OF POLYSACCHARIDE CONTAINING MATERIALS
FILE REFERENCE: 00/20910
CURRENT FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
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| LOCATION: (1)..(263)
| OTHER INFORMATION: protein A from cloning vector NAME/KEY: misc_feature
| LOCATION: (265)..(426)
| OTHER INFORMATION: CBPA | PCT-US00-00708-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE----
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------FGFASGRATL
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US-09-808-898-22
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Search completed: November 5, 2003, 20:25:13 Job time : 218.976 secs
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                                                                                                                                                      0; Gaps
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                                                                                                         Query Match 35.7%; Score 477; DB 7; Length 162; Best Local Similarity 97.8%; Pred. No. 4.7e-41; Matches 90; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shoseyov, oded
APPLICANT: Shoseyov, oded
APPLICANT: Shpiegl, Etai
APPLICANT: Roiz, Levasa
APPLICANT: Roiz, Levasa
TITLE OF INVENTION: METHODS FOR USE OF A CELLULOSE
TITLE OF INVENTION: BINDING DOMAIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: El PR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,588
FILING DATE: To be assigned
PRIOR.APPLICATION DATA:
APPLICATION NUMBER: 08/537,893
FILING DATE:
                                                                                                                                                                                                                                                                                                         66 LGNSYVDNTSKVTANFVKETASPISTYDTYVE 97
                                                                                                                                                                                                                                                                                  61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US94/04132
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MISROCK, S. LESILE
REFERENCE/DOCKET NUMBER: 7809-017
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                             US-08-962-588-2; Sequence 2, Application US/08962588; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: TENGTH: 162 amir-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 162 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 97.8
Matches 90; Conservative
                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-330-394-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-962-588-2
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APPLICANT: Hernan, Ronald A
APPLICANT: Mehigh, Richard J
APPLICANT: Mehigh, Richard J
APPLICANT: Mehigh, Richard J
APPLICANT: Brockie, Ian
APPLICANT: Brockie, Ian
APPLICANT: Brockie, Ian
APPLICANT: Jenkins, Elizabeth
TITLE OF INVENTION: Affinity Peptides and Method for Purification of Recombinant Prot
FILE REFERENCE: SGM 7047.1
CURRENT APPLICATION NUMBER: US 60/388,059
RRIOR APPLICATION NUMBER: US 60/388,059
RRIOR APPLICATION OS: 23
SOFTWARE: PATENTING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRY-YYTSDGTQGQTFWCDHAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 34.9%; Score 466.5; DB 30; Length Best Local Similarity 96.8%; Pred. No. 6e-40; Matches 90; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 LLGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
66 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Clostridium cellulovorans
                                                                                   RESULT 15
US-10-460-524-2
; Sequence 2, Application US/10460524
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 163
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 5, 2003, 20:13:32 ; Search time 14:5907 Seconds (without alignments) 824.821 Million cell updates/sec Run on:

Perfect score:

US-09-677-374-6 1335 1 MSVEFYNSNKSAQTNSITPI......IYGTACPQPDGRWQVISTEK 256 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 248976 segs, 47010500 residues Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptcdata/2/paa/USO6\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptcdata/2/paa/USO6\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptcdata/2/paa/USO8\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptcdata/2/paa/USO9\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptcdata/2/paa/USO9\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptcdata/2/paa/USO9\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptcdata/2/paa/USO8\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                | 9,               | Sequence 4, Appli                    | 7                | 29, 1             | 328                | 16, 7             | Sequence 434, App  | 309,               |                     |                      | _                 | 7766,               | 114, 2             | Sequence 8, Appli |                    | Sequence 174, App  | 14893               |                      | Sequence 59685, A    | Sequence 70443, A    | Sequence 2, Appli | 1578                | 4944                 | 27,               | Sequence 27, Appl |
|----------------------------|------------------|--------------------------------------|------------------|-------------------|--------------------|-------------------|--------------------|--------------------|---------------------|----------------------|-------------------|---------------------|--------------------|-------------------|--------------------|--------------------|---------------------|----------------------|----------------------|----------------------|-------------------|---------------------|----------------------|-------------------|-------------------|
| ID                         | US-10-261-445B-6 | US-10-241-443B-4<br>US-10-241-602B-6 | US-10-261-445B-2 | US-09-955-555B-29 | PCT-US03-19153-328 | US-10-261-445B-16 | US-09-581-286A-434 | US-09-581-286A-309 | US-09-897-516A-5133 | US-10-425-114A-61312 | US-10-389-647-605 | US-09-897-516A-7766 | PCT-US03-21510-114 | PCT/US02/39429-8  | US-60-487-610-1870 | PCT-US02-35624-174 | US-10-679-063-14893 | US-10-425-114A-51273 | US-10-425-114A-59685 | US-10-425-114A-70443 | PCT-US03-19834-2  | US-10-679-063-15782 | US-10-425-114A-49440 | PCT-US03-28626-27 | US-10-661-398-27  |
| DB                         | 9                | o o                                  | 9                | 'n                | -                  | 9                 | ហ                  | വ                  | 'n                  | 9                    | 9                 | Ŋ                   | Н                  | Н                 | 7                  | <del>, -4</del>    | 9                   | 9                    | 9                    | 9                    | ٦                 | 9                   | 9                    | Н                 | 9                 |
| %<br>Query<br>Match Length | 256              | 162                                  | 162              | 599               | 499                | 20                | 223                | 230                | 106                 | 363                  | 66                | 403                 | 1117               | 423               | 683                | 1397               | 272                 | 296                  | 345                  | 521                  | 3011              | 497                 | 734                  | 1327              | 1327              |
| &<br>Query<br>Match        | 100.0            | 61.0                                 | 61.0             | 18.4              | 9.3                | 8.4               | 7.7                | 7.7                | 7.1                 | 6.5                  | 6.5               | 6.5                 | 6.5                | 6.3               | 6.3                | 6.3                | 6.3                 | 6.2                  | 6.2                  | 6.2                  | 6.2               | 6.2                 | 6.2                  | 6.2               | 6.2               |
| Score                      | 1335             | 815                                  | 815              | 245               | 124                | 112               | 102.5              | 102.5              | 94.5                | 87                   | 86.5              | 86.5                | 86.5               | 84                | 83.5               | 83.5               | 83                  |                      | 83                   | 83                   | 83                | 82.5                | 82.5                 | 82.5              | 82.5              |
| Result<br>No.              |                  | 9 M                                  | 4                | ß                 | 9                  | 7                 | 8                  | 6                  | 10                  | 11                   | 12                | . 13                | 14                 | 15                | 16                 | 17                 | 18                  | 19                   | 20                   | 21                   | 22                | 23                  | 24                   | 25                | 56                |

| Sequence 1669, Ap<br>Sequence 23425, A<br>Sequence 16542, A<br>Sequence 2863, Ap<br>Sequence 3014, Ap          | Sequence 95, Appl<br>Sequence 8, Appli<br>Sequence 8, Appli<br>Sequence 73075, A<br>Sequence 50, Appl | Sequence 24, Appl<br>Sequence 58, Appl<br>Sequence 22, Appl<br>Sequence 22745, A<br>Sequence 22744, A | Sequence 120, App<br>Sequence 406, App<br>Sequence 256, App<br>Sequence 3444, Ap    |
|--|---|---|---|
| US-09-674-546A-1669<br>US-10-679-063-23425<br>US-10-679-063-16542<br>PCT-US03-28227-2863<br>US-60-478-196-3014 | PCT-USO2-35624-95<br>US-10-009-002-5<br>US-10-089-278-8<br>US-10-425-114A-73075<br>US-10-435-696-50   | US-10-689-006-24<br>US-09-408-020-58<br>PCT-US02-39429-88<br>US-10-679-063-22744                      | PCT-US03-19153-120<br>US-10-296-734-406<br>US-60-502-656-256<br>PCT-US03-26780-3444 |
| 11665  | 4 9 9 9 9   | φυ-ιφφ  | 1961  |
| 2599<br>595<br>1261<br>293<br>515  | 1016<br>3033<br>330<br>435<br>593   | 261<br>222<br>438<br>515<br>517   | 852<br>3011<br>2871<br>1755   |
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| 82.5<br>82.5<br>80.5<br>80   | 80<br>79.5<br>79<br>79  | 78.5<br>78<br>78<br>78  | 78<br>78<br>77.5  |
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# ALIGNMENTS

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APPLICANT: Burtan, Jan
APPLICANT: Burtan, Jan
APPLICANT: Burtan, Jan
APPLICANT: Ray, William W.
APPLICANT: Thorncon, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64095
CURRENT APPLICATION NUMBER: US,10/261,445B
CURRENT FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATCHIN VORTSION 3.0
SOFTWARE: PATCHIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 EKVKAGQVTRWRNPDTGNSYSVEPVRTYQRTNKQERRQQYCREFQQKAMIAGQKQEIYGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1335; DB 6;
100.0%; Pred. No. 1.5e-112;
ive 0; Mismatches 0;
                     Sequence 6, Application US/10261445B
GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SIGNAL
LOCATION: (-95)..(-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-261-445B-6
US-10-261-445B-6
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241 ACPQPDGRWQVISTEK 256

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Gaps

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Length 162; Indels 62

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157 GGLIGSKIGQSMDQODKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                                                                                            RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                              97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                       217 ROQYCREFOOKAMIAGOKOEIYGTACPOPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                  123 RÓGYCREFŐGKAMIAGÓKOEIYGTACRÓPDGRWQVISTEK 162
                                                                                                        Query Match 61.0%; Score 815; DB 6; L
Best Local Similarity 98.8%; Pred. No. 5.1e-66;
Matches 158; Conservative 1; Mismatches 1;
                    TYPE: PRT ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-955-555B-29
                                               ; ORGANISM: F1:
US-10-241-602B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-261-445B-2
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  LENGTH: 162
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                                                                                                                                                                                          APPLICANT: Margh, Jan. APPLICANT: Ray, William W.
APPLICANT: Ray, William W.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REPERENCE: 4616-64095
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR PLING DATE: 2000-09-15
PRIOR PAPLICATION NUMBER: US 60/577,374
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 4
LENGTH: 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 LGGLIGSKIGQSMDQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYKQE 120
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APPLICANT: Jones, Simon
APPLICANT: Griffiths, Steve
APPLICANT: Valenzuela, Pablo
APPLICANT: Burzio, Luis
TITLE OF INVENTION: Sequences from Piscirickettsia salmonis
FILE REFERENCE: H-32319A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
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CURRENT FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: US/10/241,602B
CURRENT FILING DATE: 2002-09-11
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2000-03-11
PRIOR FILING DATE: 2000-07-01
PRIOR FILING DATE: 2000-07-01
PRIOR PELING DATE: 2000-07-01
PRIOR APPLICATION NUMBER: GB0016080.4
PRIOR FILING DATE: 2000-07-01
PRIOR FILING DATE: 2000-07-01
PRIOR FILING DATE: 2000-07-01
PRIOR FILING DATE: 2000-07-05
SEQ ID NOS: 34
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10241602B
GENERAL INFORMATION:
APPLICANT: Simard, Nathalie
                                                                                                                               Sequence 4, Application US/10261445B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Piscirickettsia salmonis
241 ACPQPDGRWQVISTEK 256
                                                                                                                                                                            APPLICANT: Kuzyk, Michael A.
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US-10-241-602B-6
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APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCIRES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
CURRENT APPLICATION NUMBER: US/10/261,445B
CURRENT FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROOYCREFOOKAMIAGOKOEIYGTACPOPDGRWOVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 ROQYCREFQOKAMIAGOKQEIYGTACROPDGRWOVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/0995555B
GENERAL INFORMATION:
APPLICANT: Bott, Richard R.
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Liu, Chung-Cheng
APPLICANT: Liu, Chung-Cheng
APPLICANT: Mard, Michael
Sequence 2, Application US/10261445B; GENERAL INFORMATION:
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LENGTH:
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GENERAL INFORMATION:
APPLICANT: Diversa Corporation
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM AND
TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 09010-290W01
CURRENT APPLICATION NUMBER: PCT/US03/19153
CURRENT FILING DATE: 2003-06-16
PRIOR PLICATION NUMBER: US 60/389,299
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 378
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 328
LENGTH: 499
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                  TITLE OF INVENTION: Enzymatic Array and Process of Making TITLE OF INVENTION: Same FILE OF INVENTION: Same CREATER SEPREMENTS: GC278-C3 CURRENT FILING DATE: 2001-09-17 PRIOR APPLICATION NUMBER: US 60/005,701 PRIOR PILING DATE: 1995-11-17 PRIOR FILING DATE: 1995-11-17 PRIOR FILING DATE: 1995-11-17 PRIOR FILING DATE: 1995-10-17 PRIOR FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.4%; Score 245; DB 5; Length 599; Best Local Similarity 51.5%; Pred. No. 5.4e-14; Matches 53; Conservative 16; Mismatches 30; Indels
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9.3%; Score 124; DB 1; Length 499;
Best Local Similarity 33.0%; Pred. No. 0.0033;
Matches 33; Conservative 14; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LGN -- SYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Obtained from an environmental sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCL 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Clostridium thermocellum
US-09-955-5558-29
Xia, Hai-Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAME/KEY: SIGNAL
LOCATION: (1) ... (29)
PCT-US03-19153-328
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APPLICANT:
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APPLICANT: BUTIAN, Jan
APPLICANT: BUTIAN, JAN
APPLICANT: KAY, William W.
APPLICANT: KAY, WILLIAM W.
APPLICANT: TAO, WILLIAM W.
APPLICANT: TOOL JULIAN W.
APPLICANT: TOOL JULIAN W.
APPLICANT: TOOL JULIAN W.
APPLICANT: TITLE OF INVENTION: VACINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64095
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR PELLING DATE: 2000-09-15
PRIOR PELLING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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NUMBER OF SEQ ID NOS: 721
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THIS MEKEKENIE, 413/1.

CURRENT FILING DATE: 2000-06-28

PRIOR APPLICATION NUMBER: US/09/581,286A

PRIOR FILING DATE: 1998-12-10

PRIOR PILING DATE: 1998-12-10

PRIOR PILING DATE: 1997-12-10

PRIOR APPLICATION NUMBER: AU PP 1182

PRIOR APPLICATION NUMBER: AU PP 1182

PRIOR PILING DATE: 1997-12-31

PRIOR PILING DATE: 1998-03-10

PRIOR PILING DATE: 1998-03-10

PRIOR PILING DATE: 1998-03-10

PRIOR PELING DATE: 1998-03-10

PRIOR PELING DATE: 1998-03-10

PRIOR PELING DATE: 1998-04-09

PRIOR PELING DATE: 1998-04-09

PRIOR PELING DATE: 1998-04-09

PRIOR PELING DATE: 1998-04-09

PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-06-05

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PRIOR PELING DATE: 1998-06-05

PRIOR PELING DATE: 1998-06-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 PVRTYQRYNKQERRQQYCRE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Piscirickettsia salmonis
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APPLICANT: BARR, IAN G.
APPLICANT: PATTERSON, MICHELLE A.
APPLICANT: AGIUS, CATHERINE T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROTHEL, LINDA J.
MARGETTS, MAL B.
HOCKING, DIANNA M.
WEBB, ELIZABETH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin version 3.2
SEQ ID NO 434
LENGTH: 223
Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
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TYPE: PRT
ORGANISM: Zea mays
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LENGTH: 363
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                                                                                                                                             103 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSM-AIGGAVLGGLIG 161
                                                                                                                                                                                 8 ASVLAVALVFAGCGIN--NMAKĞGLIĞAĞGYĞGAIĞAĞVĞNVAĞNTAVĞAIVĞTAVĞGAAĞ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSM-AIGGAVLGGLIG 161
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APPLICANT: MARGETTS, MAL B.
APPLICANT: HOCKING, DIANNA M.
APPLICANT: WEBB, ELIZABETH A.
TITLE OF INVENTION: PORPHORYMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
FILE REFERENCE: 4137-3
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NUMBER OF SEQ ID NOS: 721
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                                                Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 230;
                                                                                                    Indels
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                                                   DB 5;
                                                                                                 31;
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                                              Query Match 7.7%; Score 102.5; DB Best Local Similarity 34.7%; Pred. No. 0.099; Matches 25; Conservative 13; Mismatches 3
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TLUE KEFEKENCE; 41.27.

CURRENT PELING DATE: 2000-06-28

PRIOR APPLICATION NUMBER: US/09/581,286A

PRIOR FILING DATE: 1998-12-10

PRIOR PILING DATE: 1998-12-10

PRIOR PELING DATE: 1997-12-10

PRIOR PELING DATE: 1997-12-30

PRIOR PELING DATE: 1997-12-31

PRIOR PELING DATE: 1998-01-30

PRIOR PILING DATE: 1998-04-09

PRIOR PILING DATE: 1998-04-09

PRIOR PILING DATE: 1998-04-09

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PRIOR PILING DATE: 1998-04-09

PRIOR PILING DATE: 1998-04-03

PRIOR PILING DATE: 1998-04-03

PRIOR PILING DATE: 1998-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 309, Application US/09581286A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: AU PP 3654
PRIOR APPLICATION NUMBER: AU PP 3654
PRIOR PELICAD DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Porphyromonas gingivalis
US-09-581-286A-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROSS, BRUCE C.
PAPLICANT: BARK, IAN G.
APPLICANT: PATTERSON, MICHELLE A.
APPLICANT: AGIUS, CATHERINE T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin version 3.2
SEQ ID NO 309
LENGTH: 230
                                                                                                                                                                                                                                              162 SKIGQSMDQQDK 173
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66 ALIGKKMDKQKK 77
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73 ALIGKKMDKQKK 84
US-09-581-286A-434
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RESULT 11
US-10-425-114A-61312
; Sequence 61312, Application US/10425114A
; Sequence 61312, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 191313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 TYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 QTFGAILGAVAGSVVGYNAGSGSGAGTAAGAVGGGALGAAAGSVVKDKVIVEGVSLTYKE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 SILNRNSFRCEEIRAYST---TQACTYACAHAGT-----RTRRIGLSLSLQTHDDEP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 DTQQY----HIHTLQA-----ALDQAACRPNASSSDV-----AVAGAL-GRHGG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 SDLNLNDVK---VRYYYTSDGTQGQTFWCDHAGALLGNSYVDNTSKVTANFVKETASPTS
                                                                                                                                                                                                                                                                           APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFRESENCE: 38-21(51847)8
CURRENT APPLICANN UNMERS: US/09/897,516A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 QEVGAATGAVVGGVAGQLFGKGS--GRVSMAIGGAVLGGLIGSKI---
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US-10-425-114A-61312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94.5; DE Pred. No. 0.2; 9; Mismatches
                                                          APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Krasomil-Osterfeld, Karina C.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/215,161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8415
; Sequence 5133, Application US/09897516A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 KTKIYTSTQVGRTCQFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.1%;
Best Local Similarity 35.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 KIKLNOSLEKVKAGOVT
                                                                                                                                                                                                                                                     Slater, Steven C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Xenorhabdus sp.
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63 DLSLKDPLMLAFFATVGLNANLASLRAGGKLL--LIFVVAVVGLLLVQNTVGIALAKML 119
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20.8%; Pred. No. 22;
tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 -----IKLNQSLEKVKAG------
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PCT/US02/39429-8
; SEQUENCE 8, Application PC/TUS0239429
; GENERAL INFORMATION:
; APPLICANT: NeoRx Corporation
; APPLICANT: Gosborn, Stephen Charles
; APPLICANT: Schultz, Joanne Blaine
; APPLICANT: Lin, Yukang
; APPLICANT: Lin, Yukang
; APPLICANT: Seno, John M.
; APPLICANT: Beno, John M.
; APPLICANT: Dearstyne, Erica A.
                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US03-21510-114
; Sequence 114, Application PC/TUS0321510
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Conservative
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Matches 52; Conserv
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Huesing, Joseph E.
APPLICANT: Huesing, Joseph E.
APPLICANT: Slacer, Steven C.
APPLICANT: Slacer, Steven C.
APPLICANT: Slacer, Serven C.
APPLICANT: Slacer, Slacer, Serven C.
APPLICANT: Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slacer, Slace
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                                                                                                                                                                                                                                                              Sequence 605, Application US/10389647
GENERAL INFORMATION:
APPLICANT: GREENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: COSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REFERENCE: U12-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT APPLICATION NUMBER: 09/653730
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 710
SEQ ID NO 65
SEQ ID NO 65
LENGTH: 99
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GENERAL INFORMATION:
APPLICANT: Corbin, David R.
                                 146 RVSMAIGGAVLGGLIGSKIGQS 167
                                                                                                 94 AVAVAİĞAVVVDĞVAAPDLĞQA 115
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; ORGANISM: Pseudomonas aeruginosa
US-10-389-647-605
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APPLICANT: EXELIXIS,
TITLE OF INVENTION:
TITLE OF INVENTION: MP21S AS MODIFIERS OF THE p21 PATHWAY AND METHODS OF USE
FILE REFERENCE: EXO3-06C-PC
CURRENT APPLICATION NUMBER: PCT/US03/21510
CURRENT FILING DATE: 2003-07-09
PRIOR PILING DATE: 2002-07-10
PRIOR FILING DATE: 2002-07-10
PRIOR PILING DATE: 2002-07-10
PRIOR FILING DATE: 2002-09-08
PRIOR FILING DATE: 2002-09-08
PRIOR PILING DATE: 2002-09-16
PRIOR PILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-12-30
PRIOR FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 124
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90 YLDPSHMRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFG-KGSGRVS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 VSSSGSPASVMTNMRAPSTTGGIGINSVTGTSTVNNVNITAVGSFNPNVTSSILGNVNIS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 RQEVGAATGAVVG-GVAGQ-----LFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDK- 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 SERESTSGSSVS-SSVSTLSHYTESVGSGEMGAPTVVVQQQQQQQQQQQQPALQGVTLQ 562
                                                        120 GLDP--LMGLLAG-----SVTLSG-----GHGTGAAWGKVFTERYGFENATEVA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 VKETASPISTYDTYLDPSHMRG----CLQGSSLI-IISVFLVGCAQ------NFS
                                                                                                                                                             149 MAIG--GAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1117;
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TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.54701PC
CURRENT APPLICATION UNMBER: PCT/US02/39429
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PRT
ORGANISM: Artificial Sequence
FENTURE:
FENTURE:
GRANDISM: Artificial Sequence
CTARE INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- gence
PCT/US02/39429-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 DPSHMRGCLQGSSLIIISVFLVGCAQ----NFSRQEV-GAATGAVVGGVAGQLFGKGSG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 RVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL------EKV------- 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.3%; Score 84; DB 1; Length 423; Best Local Similarity 25.2%; Pred. No. 10; Matches 55; Conservative 22; Mismatches 73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 F--OQKAMIAGOKORI----YGTACPOPDGRWQVISTE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: November 5, 2003, 20:25:59 Job time: 15.5907 secs
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November 5, 2003, 20:06:21; Search time 29.3782 Seconds (without alignments) 875.264 Million cell updates/sec
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| SIDSI]gcgdata/geneseqg/geneseqg-embl/AA419991.DAT:*
| SIDSI]gcgdata/geneseqg/geneseqg-embl/AA419991.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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| Ş | G         | X  | PF    | X           | PR      | PR                 | PR                 | PR                 | ×                  | PA                 | X                  | ΡI                 | ΡΙ                 | X                  |  |
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|   |           |    |       |             |         |                    |                    |                    |                    |                    |                    |                    |                    |                    |  |
|   |           |    |       | Description |         | Piscirickettsia sa | OspA antigen amino | Piscirickettsia sa | Optimised OspA pro | Escherichia coli c | C17E2 OspA constru | E. coli codon opti | Pseudomonas aerugi | OspA B-cell epitop |  |
|   | SUMMARIES |    |       | ID          |         | AAG78025           | AAB81126           | AAU97867           | AAB81127           | AAU97868           | AAB81128           | AAU97869           | ABJ18820           | AAB81130           |  |
|   |           |    |       | DB          | -       | 22                 | 22                 | 23                 | 22                 | 23                 | 22                 | 23                 | 24                 | 22                 |  |
|   |           |    |       | Length      | 1 1 1 1 |                    |                    |                    |                    |                    |                    | 256                |                    |                    |  |
|   |           | do | Query | Match       |         | 100.0              | 100.0              | 100.0              | 97.5               | 97.5               | 97.5               | 97.5               | 15.4               | 13.4               |  |
|   | ٠         |    |       | Score       |         | 836                | 836                | 836                | 815                | 815                | 815.               | 815                | 128.5              | 112                |  |

Griffiths S, Valenzuela P;

Brouwers H, Jones S,

Simard N, Burzio L;

RESULT 1
AAG78025
ID AAG78025 standard; Protein; 162 AA.
XX
AC AAG78025 standard; Protein; 162 AA.
XX
AC AAG78025;
XX
DT 15-JAN-2002 (first entry)
XX
DT Spirickettsia salmonis; piscirickettsiosis; salmonid rickettsial;
XX
DE Piscirickettsia salmonis; piscirickettsiosis; salmonid rickettsial;
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Piscirickettsia salmonis.
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This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA, in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents P. salmonis ospA protein. An OspA protein with an Alternian fusion partner is used in a vaccine to create an anti-OspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                1 MARGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
                                                                                                                                                                                                                                                                                                                                                                                                         1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia;
containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                  Length 162;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piscirickettsia salmonis outer surface lipoprotein OspA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 836; DB 22;
100.0%; Pred. No. 3.8e-80;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burian J,
                                        Example 2; Fig 2B; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-2000; 2000US-0677374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piscirickettsia salmonis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (THOR/) THORNTON J C. (KAYW/) KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettisial disease.
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                                                                                                                                                                                                                                                                                                   162 AA;
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BURIAN J.
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                                                                                                                                                                                                                                                                                                                                                                                                                              MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA 60
                                                                                                                                                                    The invention relates to nucleic acid sequences and the encoded protein of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity to protect fish against P. salmonis which causes piscirickettsiosis, also known as salmonid rickettsial septicaemia.
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                                                                                                                                                                                                                                                                                                                                                                                             1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poikilothermic fish, Piscirickettsia salmonis, rickettsial pathogen;
vaccine, OspA, salmonid rickettsial septicaemia, rickettsial disease;
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                             New nucleic acids encoding an amino acid sequence homologous to the surface antigen present on Piscirickettsia salmonis are useful to protect fish against piscirickettsiosis
                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                      Length 162;
                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                    ; Score 836; DB 22;
; Pred. No. 3.8e-80;
0; Mismatches 0;
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/label= B_cell_epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OspA antigen amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB81126 standard; Protein; 162
                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                        Claim 6; Fig 5; 25pp; English.
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                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-316844/34.
         2001-639050/73.
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(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                      162 AA;
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                            N-PSDB; AAH79040.
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AAB81126 RESULT

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Thornton JC,
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                  The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piecirickettsia Salmonis comprising administering either intraperitoneally, by immersion or oxally, an immunogenic amount of principal antigen, the OspA (outer series [ipoprotein], its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septiceemia and other related fickettisial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Piscirickettsia salmonis outer surface lipoprotein, OspA, used in the creation of the vaccine described is the incompleted of the piscirickettsia salmonis outer surface lipoprotein, OspA, used in the creation of the vaccine described
                                                                                                                                                                                                                                                                                                     61 VLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ 120
                                                                                                                                                                                                                                                                                       61 VLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ 120
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                                                                                                                                                                                                                                                         1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA 60
                                                                                                                                                                                                                                           1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poikilothermic fish, Piscirickettsia salmonis, rickettsial pathogen, vaccine, OspA, salmonid rickettsial septicaemia, rickettsial disease,
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                      .
                                                                                                                                                                                                Length 162;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                   ERROQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                             100.0%; Score 836; DB 23;
100.0%; Pred. No. 3.8e-80;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Optimised OspA protein 17E2 amino acid sequence.
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109..128
                                                                                                                                                                                                                                                                                                                                                                                                             AAB81127 standard, Protein, 161 AA.
 Claim 15; Fig 2; 55pp; English.
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Matches 162, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-316844/34.
N-PSDB; AAF86247.
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KUZYK M A.
                                                                                                                                                                           162 AA;
                                                                                                                                                      in the invention.
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                                                                                                                                                                           Sequence
                                                                                                                                                                                                  Query Match
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(KUZY/) |
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                                                                                                                                                                             This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia asalmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed 05pA, or an immunogenic fragment of 0spA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents optimised P. salmonis OspA protein 1782. The DNA encoding OspA 1782 (Angles Deen optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
Method for protecting poikilothermic fish against salmonid rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                           septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease; 17e2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.5%; Score 815; DB 22; Length 161; 98.8%; Pred. No. 6.3e-78; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli codon optimised OspA, 17e2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU97868 standard; Protein; 161 AA
                                                                                                                                Disclosure; Fig 5; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 158; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (THOR/) THORNTON J C. (KAYW/) KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-455221/49.
N-PSDB; ABK52402.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 AA;
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                                                              The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity in fin-fish against Rickettsial septicaemia and other related Rickettsial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) used in the creation of the vaccine
                                                                                                                                                                                                                                                                                                                                          GGLIGSKIGOSMDOODKIKLNOSLEKVKAGOVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                       GGLIGSKIGOSMDQODKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96..256
/label= C17E2 OspA
/note= "Product of OspA gene optimised for expression in
Escherichia coli"
                                                                                                                                                                                                                                                                                                          RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poikilothermic fish, Piscirickettsia salmonis, rickettsial pathogen, vaccine, OspA, salmonid rickettsial septicaemia, rickettsial disease, SRS, 17E2; fusion construct.
                                                                                                                                                                                                                                                                        Gaps
Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
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                                                                                                                                                                                                                                                Length 161;
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|Tabel= Undefined_N-terminal_fusion_partner
                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C17E2 OspA construct with N-terminal fusion partner.
                                                                                                                                                                                                                                                Score 815; DB 23;
Pred. No. 6.3e-78;
1; Mismatches 1;
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                                              Example 4; Fig 5; 55pp; English.
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                                                                                                                                                                                                      described in the invention.
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Synthetic.
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.8
Matches 158; Conservative
                       strain, as a vaccine
                                                                                                                                                                                                                            161 AA;
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                                                                                                                                                                                                                              Sequence
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This invention relates to a method for the protection against infection of a poixilothermic fish by the bacterial pathogen, Piscirickettsia asalmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed 05pA, or an immunogenic fragment of 0spA in the form of a vaccine. The method is used for protecting animals, particularly poixilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonia rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a P. salmonis OspA construct optimised for expression in Bscherichia coli, fused to an undefined N-terminal fusion patriner. The fusion protein is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGLIGSKIGQSMDQODKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGLIGSKIGQSMDQQDKIKINQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                                                                                                Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E. coli codon optimised OspA, 17e2 with N-terminal fusion peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease; 17e2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROOYCREFOOKAMIAGOKOEIYGTACROPDGRWOVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROQYCREFQOKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 815; DB 22;
Pred. No. 1.1e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU97869 standard; Protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 5; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.5%;
                                                                                      Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-2001; 2001CA-2339327.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (THOR/) THORNTON J C. (KAYW/) KAY W W.
                                                                                      Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 AA;
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                               N-PSDB; AAF86248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA2339327-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                         Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU97869
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modulating biofilm formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating biofilm formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by bacteria or modularing bacterial antibiotic resistance. The method of the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is afflicted with a biofilm-associated disease or disorder, such as: cystic fibrosis; AIDS; middle ear infections, anchy periodontal disease; catheter-associated infections, and medical device-associated infections. The present amino acid sequence represents a protein that is used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 QIAGTAIGAVVGGLLGNQIGGGTGKKIATVAGAVGGGYAGNKVQEGMQERDTYTTTETRC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a
                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises a method for identifying a compound capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 QEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; antibody.
                                                                                                                                                                                                                         Identifying compound capable of modulating biofilm formation by bacteria/bacterial antibiotic resistance, useful for treatment of biofilm associated disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.4%; Score 128.5; DB 24; Length 182; 34.8%; Pred. No. 2.1e-05; Live 13; Mismatches 28; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 -KLNQSLEKV-----KAGQVTRWRNP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 STVHDSSEKVVGYDVKYMLDGKAĞQIRMERDP 161
                                                                    Greenberg
                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 152; 154pp; English.
                                                                    တွဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OspA B-cell epitope peptide #2.
                                                                    Lory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB81130 standard; Peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kuzyk MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99CA-2281913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 34.89
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                                                                 Bangera MG,
(HARD ) HARVARD COLLEGE.
                                                                                                                                   WPI; 2003-075601/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-316844/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAY W W.
BURIAN J.
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                                                                                                                                                              N-PSDB; ABT14642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA2281913-A1
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                                                                 Whiteley M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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(KUZY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRAKE SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Pisciricketteia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the Osph (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (Osph) of bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in fin-fish against Rickettsial septicaemia and other related Rickettisial diseases caused by either a virus, bacteria or parasite. This is the amino acid sequence of the Escherichia coli codon optimised outer surface lipoprotein OspA (17e2) with an N-terminal fusion used in the creation of the vaccine described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biofilm formation modulation; biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection; acne; periodontal disease; catheter-associated infection; medical device-associated infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                        Inducing immunity in fin fish to Rickettsial septicaemia, comprises administration of an outer surface lipoprotein (OspA) of a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.5%; Score 815; DB 23; Length 256; 98.8%; Pred. No. 1.1e-77; ive 1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
                                                                                                    Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ź
                                                                                                    Burian J,
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                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Fig 5; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2001; 2001US-285190P.
24-OCT-2001; 2001US-344142P.
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                                                                                             Thornton JC, Kay WW,
                                                                                                                                                                                                                                                                                                                                strain, as a vaccine
                                                                                                                                                              WPI; 2002-455221/49.
N-PSDB; ABK52403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                  (KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 AA;
BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200285295-A2
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63

Query Match

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ABJ18820

80

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Length 20; Indels

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bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity
                      in fin-fish against Rickettsial septicaemia and other related Rickettisial diseases caused by either a virus, bacteria or parasite. This sequence represents a synthetic peptide used to create polyclonal rabbit antibodies against the Piscirickettsia salmonis outer surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moraxella, vaccine, respiratory tract infection, antiinflammatory, auditory; antibacterial; otitis media, sinusitis; pneumonia.
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                                                                                                                                                                                                               Score 112; DB 23; Pred. No. 6.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M catarrhalis MCA100414 protein SEQ ID NO: 10.
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                      110 PVRTYQRYNKQERRQQYCRE 129
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                                                                                                                                                                                                                                                                                                                                                                                                        1 PVRTYORYNKOERROOYCRE
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2000US-228742P.
2000US-228773P.
2000US-229465P.
2000US-229474P.
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2000US-228443P.
2000US-228441P.
2000US-228442P.
2000US-228443P.
2000US-228443P.
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2000US-229803P.
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2000US-228296P.
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                                                                                                                                                                                                                                                                                                      Conservative
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N-PSDB; AAL46497.
                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                      lipoprotein, OspA.
                                                                                                                                                                                         20 AA;
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29-AUG-2000;
29-AUG-2000;
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29-AUG-2000;
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29-AUG-2000;
29-AUG-2000;
01-SEP-2000;
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                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                       This invention relates to a method for the protection against infection of a poixilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed 08pA, or an immunogenic fragment of 08pA in the form of a vaccine. The method is used for protecting animals, particularly poixilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents an immunogenic epitope of the P. salmonis OspA protein. The peptide is used to raise rabbit anti-OspA antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a method of protecting a poikilothermic fish against infection by the bacterial pathogen Piscirickettsia Salmonis comprising administering either intraperitoneally, by immersion or orally, an immunogenic amount of principal antigen, the OspA (outer surface lipoprotein), its variants, non-lipidated form or antigenic peptides derived or synthesized with or without an adjuvant. The new method is used to provide an outer surface lipoprotein (OspA) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer surface lipoprotein; OspA; antibacterial; immunosupressive; vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia; Rickettisial disease.
     containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 112; DB 22;
Pred. No. 6.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Outer surface lipoprotein OspA based peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burian J, Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 13.4%; Score 112; DE 1. Similarity 100.0%; Pred. No. 6.9
20; Conservative 0; Mismatches
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                                                          Example 2; Page 17; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 PVRTYQRYNKQERRQQYCRE 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THORNTON J C.
KAY W W.
BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thornton JC, Kay WW,
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Best Local Similarity
Matches 20; Conserv
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(BURI/)
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N-PSDB; ABS66202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG80432;
                                                                                                                                     Sequence
                                                                                                                                                                    Query Match
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                                                                                                                The present invention provides the protein and coding sequences of proteins from Moraxella catarrhalis. These can be used to produce accines which protect against M. catarrhalis infection, which can cause otitis media, respiratory infection, sinusitus, and pneumonia. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                             8 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVAMAIGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium, useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia
                                                                                                                                                                                                                                                                                                                                                              7 GVVLLASSMALAGCANTGT---TGNGTGFGGANVNKAVIGAVAGAL---GGTAISKATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASB113 polypeptides, and polymucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB113 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASB113 polypeptide, an immunogenic fragment of a BASB113 polypeptide, or a polypeptide having at least 85% amino acid sequence identity to BASB113, or comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of BASB113 protein from Moraxella catarrhalis strain Mc2931 (ATCC 43617), a causative agent of otitis media in children and pneumonia in adults. The invention provides
                                                                                                                                                                                                                                                                                                                                                                                                                      60 -----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASB311; infection; otitis media; pneumonia; therapy; diagnosis; antibacterial; antimicrobial.
                                immunizing a host e.g. humans against disease e.g. otitis media, pneumonia, caused by infection of the bacteria
                                                                                                                                                                                                                                                           12.9%; Score 108; DB 23; Length 197; 32.4%; Pred. No. 0.0033;
                  Moraxella polypeptide and polynucleotides useful as vaccine
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moraxella catarrhalis BASB113 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 67; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB20105 standard; Protein; 224
                                                                                 Claim 28; Fig 9; 277pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99GB-0015044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-2000; 2000WO-EP05851
                                                                                                                                                                                                                                                                           Local Similarity 32.4 tes 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-112458/12.
                                                                                                                                                                                                                          197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAF30043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200100836-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thonnard J;
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB20105;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel hyperblebbing Gram-negative bacterium that has been genetically modified by down-regulating expression of Tol genes, and/or attenuating peptidoglycan-binding activity useful for treating bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hyperblebbing, Gram-negative bacterium; genetically modified; Tol gene peptidoglycan-binding; peptidoglycan-associated site; outer-membrane; bacterial infection; vesicle-shedding; Bleb; filter sterilised; detergent; deoxycholate; homogeneity; antibacterial; vaccine; TolQ; TolA; OmpCD; xOmpA; PAL-1; PAL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVAMAIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
polynucleotide encoding such a polypeptide. A claimed method of diagnosing a Moraxella infection involves identifying a BASB113 polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection composition useful antibody directed against a BASB113 polypeptide. BASB113 polypeptides also have utility in raising specific antibodies, and in screening for antibacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 -----AVLGGLIGSKIGOSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|| :|: | : | : | | : | | EKTGRDAILGAAVGAAAGAYWERQAK.---QIEQQWQGTGVTVTHDTDTGN
                                                                                                                                                                                                                                                                                                                                                                       Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poolman J, Thonnard J;
                                                                                                                                                                                                                                                                                                                                                                       Score 108; DB 22;
Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moraxella catarrhalis PAL-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 71; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG80432 standard; Protein; 224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neyt CA,
                                                                                                                                                                                                                                                                                                                                                                           12.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moraxella catarrhalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                         224 AA;
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Gaps

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isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
(Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX91536 to AAX91801 encode two hundred and sixty six antigenic
Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to
AAY34583. AAX91802 to AAX91989 represent PCR primers used in the
                                                                                                                                                                                    9 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAM-AIGGAVLGGLIG
                                                                                                                                                                                                            ASVLAVALVFAGCGLN--NMAKGGLIGAGVGGAIGAGVGNVAGNTAVGAIVGTAVGGAAG
                                                                                                                                                           3;
                                                                                                                                 Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                gingivalis, PG, periodontal disease, gingivitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphorymonas gingivalis peptides for preventing
                                                                                                                                                           Indels
                                                                                                                       Score 105.5; DB 20;
Pred. No. 0.0072;
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                                                                                                                                                           12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       Porphorymonas gingivalis protein PG3
                                                                                                                                                                                                                                                                                                                               AAY34362 standard; Protein; 230 AA
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Webb EA;
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98AU-0001546.
98AU-0002264.
                                                                                                                                 ch 12.6%;
1 Similarity 36.1%;
26; Conservative 13
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98AU-0003128.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphorymonas gingivalis.
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                                                                                                                                                                                                                                      SKIGOSMDOODK
                                                                                                                                                                                                                                                      ALIGKKMDKOKK
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Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-385613/32
                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphorymonas ging
vaccine; antigenic
                                                                                                          223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX91580
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25-AUG-1999
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05-MAY-1998;
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10-MAR-1998
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gingivitis
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                                                                                                                                                                                                                                                                                                                                                       AAY34362;
                                                                                                                                                                                                                                       68
                                                                                                          Sequence
                                                                                                                                 Query Match
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                the use of detergents such as deoxycholate, thus obviating chromatography purification and ultra centrifugation steps. Vesicles prepared from the invention have reduced particle size (allowing sterile filtration through 0.22 mum pores), increased batch homogeneity, and a superior yield. The present amino acid sequence represents a Moraxella catarrhalis protein, as described in the invention.
                                                                                                                                                                                    8 GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVAMAIGG 59
                                                                                                                                                                                                              GVVLLASSMALAGCANTGT --- TGNGTGFGGANVNKAVIGAVAGAL --- GGTAISKATGG 60
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    The blebs can be made and harvested without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX91536 to AAX91801 encode two hundred and sixty six antigenic
Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 (
AAX34583. AAX91802 to AAX91989 represent PCR primers used in the
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                      |:|| :|: | :|| :|| EKTGRDAILGAAVGAAAGAYMERQAK----QIEQQMQGTGVTVTHDTDTGN 107
                                                                                                                                                                                                                                       60 -----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN 104
                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Porphorymonas gingivalis, PG; periodontal disease; gingivitis; vaccine; antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patterson MA;
                                                                                                                              ch 12.9%; Score 108; DB 23; Length 224; I Similarity 32.4%; Pred. No. 0.0039; 36; Conservative 16; Mismatches 35; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphorymonas gingivalis peptides for preventing
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Webb EA;
                                                                                                                                                                                                                                                                                                                               AAY34487 standard; Protein; 223
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98AU-0001546.
98AU-0002264.
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98AU-0004963.
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    filter sterilised.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphorymonas gingivalis
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Rothel LJ,
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                                                                                                                                                Local Similarity
                                                                                                         224 AA;
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30-JUL-1998;
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Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Issued Patents AA:\* Database :

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Sequence 8009, Ap Sequence 7802, Ap Sequence 6750, Ap Sequence 4442, Ap Sequence 28397, Ap Sequence 28397, Ap 2, Appli 2, Appli 3, Appli Sequence 7222, Ap Sequence 27926, A Sequence 13, Appl Sequence 8, Appli Sequence 6442, Ap Sequence 5149, Ap Sequence 6423, Ap Sequence 23878, A 19, Appl 1, Appli Sequence 21754, Sequence 23334, Sequence 31960, Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-252-91A-21754 US-09-252-91A-21334 US-09-252-991A-31960 US-09-328-352-8029 US-09-328-352-6750 US-09-328-352-6450 US-09-328-352-4442 US-09-328-352-4442 US-09-328-352-4442 US-09-252-991A-26658 US-09-252-991A-33036 US-09-328-352-7068 US-08-556-978B-19 -09-107-532A-7222 -09-252-991A-27926 -07-803-633A-13 -09-252-991A-23878 US-09-252-991A-22817 US-08-425-069-2 US-08-317-844B-2 US-09-247-806-1 -09-034-177-3 SUMMARIES Query Match Length DB 128.5 116 101.5 98.5 93.5 90 89 78.5 78.5 78 77.5 80.5 Result Š. 

US-09-553-498-8

| 8, Appli        | 7100, Ap           | 2, Appli        | 2, Appli        | 5775, Ap           | 19162, A             | 31525, A             | 26438, A             | 2, Appli         | 2, Appli        | 2, Appli         | 30059, A             | 12, Appl         | 12, Appl         | 12, Appl         | 4748, Ap            | 6584, Ap            | 23427, A             |
|-----------------|--------------------|-----------------|-----------------|--------------------|----------------------|----------------------|----------------------|------------------|-----------------|------------------|----------------------|------------------|------------------|------------------|---------------------|---------------------|----------------------|
|                 | Sequence           | Sequence        | Sequence        | Sequence           | Sequence             | Sequence             | Sequence             | Sequence         | Sequence        | Sequence         | Sequence             | Seguence         | Sequence         | Sequence         | Sequence            | Sequence            | Sequence             |
| US-09-618-869-8 | US-09-328-352-7100 | US-09-067-351-2 | US-09-360-490-2 | US-09-328-352-5775 | US-09-252-991A-19162 | US-09-252-991A-31525 | US-09-252-991A-26438 | US-08-374-077C-2 | US-08-895-590-2 | US-09-539-879A-2 | US-09-252-991A-30059 | US-07-910-760-12 | US-08-440-519-12 | US-08-440-549-12 | US-09-107-532A-4748 | US-09-107-532A-6584 | US-09-252-991A-23427 |
| 4               | 4                  | ~               | m               | 4                  | 4                    | 4                    | 4                    | ო                | ო               | 4                | 4                    | -                | Н                | 4                | 4                   | 4                   | 4                    |
| 255             | 141                | 551             | 551             | 259                | 518                  | 849                  | 1415                 | 2516             | 2516            | 2516             | 397                  | 1021             | 1021             | 1021             | 82                  | 204                 | 141                  |
| 9.3             | 9.5                | 9.5             | 9.5             | 9.5                | 9.5                  | 9.5                  | 9.5                  | 9.5              | 9.5             | 9.5              | 9.1                  | 9.1              | 9.1              | 9.1              | 9.0                 | 9.0                 | 9.0                  |
| 77.5            | 77                 | 77              | 77              | 76.5               | 76.5                 | 76.5                 | 76.5                 | 76.5             | 76.5            | 76.5             | 92                   | 92               | 26               | 16               | 75.5                | 75.5                | 75                   |
| 28              | 53                 | 30              | 31              | 32                 | 33                   | 34                   | 35                   | 36               | 37              | 38               | 39                   | 40               | 41               | 42               | 43                  | 44                  | 45                   |

### ALIGNMENTS

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Sequence 22817, Application US/09252991A
Sequence 22817, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196, 136
CURRENT APPLICATION NUMBER: US/09/252, 991A
CURRENT PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19701, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
FAPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-17
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 QEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKI----- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.4%; Score 128.5; DB 4; Length 192; 34.8%; Pred. No. 1.3e-06; vative 13; Mismatches 28; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 -KLNOSLEKV------KAGQVTRWRNP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 34.8%
Matches 32, Conservative
RESULT 1
US-09-252-991A-22817
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US-09-252-991A-19701
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Sequence 8009, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 387
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GENERAL INC. 8227/57
GENERAL INC. 8227/57
GENERAL INCORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                        11.8%; Score 98.5; DB 4; Length 387; llarity 22.1%; Pred. No. 0.0073; Conservative 26; Mismatches 47; Indels 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 SSLIIISVFLVGC---AQNFSRQEVGAATGAV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 31960, Application US/09252991A ; Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
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Best Local Similarity
Matches 38; Conserv
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Best Local Similarity
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US-09-252-991A-23334
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US-09-328-352-8009
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Sequence 21754, Application US/09252991A

Sequence 21754, Application US/09252991A

Sequence 21754, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPREBNCE: 107196.136

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21754

LENGTH: 306
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                                                                                                                                                                                                                                                                                                                                                                                                                       91 AGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ---ERRQQYCREFQOKAMIAGOKOBIYGTA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 IG-----SYGTDVDRSTVEINRSVAYAKSAÖSCYOSÖPKALLDGRKNK----S 171
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                                                                                                                                                                                                                                                                                                                                     12 MRKSALIVASFTAMALALGGCQSSLTGDTYSREEARTVQTVRMGTIQALRPVKIEGTKTP 71
                                                                                                                                                                                                                                                                                                                                                                                         30 VGAATGAVVGGVAGQLFGKGSGRVAMAİGGAVLGGLIGSKIGQSMDQQDKIKL----- 82
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                                                                                                                                                                                        Query Match
13.9%; Score 116; DB 4; Length 165;
Best Local Similarity 25.0%; Pred. No. 2.6e-05;
Matches 34; Conservative 21; Mismatches 41; Indels
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                                                                                                                                                                                                                                                                                            1 MNRGCLQGSSLIIISVFLVGC----AQNFSRQE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                     Pseudomonas aeruginosa
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Best Local Similarity
Matches 44; Conserva'
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                 NUMBER OF SEQ ID NOS:
SEQ ID NO 19701
LENGTH: 165
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                                                                                                                                          US-09-252-991A-19701
                                                                                                                     ORGANISM:
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Sequence 4253, Application US/09328352

Sequence 4253, Application US/09328352

Retent No. 6562958

GRNERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4253

LENGTH: 258
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BULMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4442
LENGTH: 730
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                                                                                                                                                                            64 MNEG---GENLVATGAGTLG------GAAVGAAFGVVGGP-----PGAVVGIIGG 105
                                                                                                                                                                                                                                      61 VLGGLIGSKIGGSMDQODKIKLNQSLEKVKAGQVTRWRNPDT--GNSYSVBPVRTYQRYN 118
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                                                                                                                                              1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
                                                                                                 Gaps
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                                                                                               41;
                                                  Length 215;
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                                                                                               Indels
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                                             10.5%; Score 87.5; DB 4; 23.5%; Pred. No. 0.057; tive 21; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.2%; Score 85.5; DB 4; 22.0%; Pred. No. 0.48; tive 30; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                   146 SEDKNLEYDRDY-RAAYRLGYENRVHNNA 173
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US-09-328-352-4442
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                                                                                                                                                                                                                                                                                     106 VVGAIAGNDİAQTNNQKD----
                                                                                          21;
                                                                                               Conservative
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                      Query Match
Best Local Similarity
Thes 35; Conserve
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  US-09-328-352-6750
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APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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APPLICANT: Gary L. Brecon et al.

APPLICANT: Gary L. Brecon et al.

APPLICANT: Gary L. Brecon et al.

TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                              9 SSLIIISVFLVGCAQNF--SRQEVGAATGAVVGGVAGQLFGKGSGR-VAMAIGGAV----
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CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                             ---LGGLIGSKIGQSM 74
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Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6750, Application US/09328352 Patent No. 6562958
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                                                                                                                   TYPE: PRT; ORGANISM: Acinetobacter baumannii
US-09-328-352-8009
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US-09-328-352-7802
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ORGANISM: Acinetobacter baumannii
                         CURRENT FILING DATE: 1999-(
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8009
LENGTH: 126
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LENGTH: 215
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Sequence 7068, Application US/09328352
Sequence 7068, Application US/09328352
Sequence 7068, Application US/09328352
Sequence 7068, Application US/09328352
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7068
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APPLICATION NUMBER:
CURRENT APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
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BRIOR FILING DATE:
1998-07-27
PRIOR FILING DATE:
1998-07-27
NUMBER OF SEQ ID NOS:
33142
LENGTH: 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GLILGGFAGE-----SLVGALLGGLSGLALGQAVSLQNLAQQNERLRKQMSBFA 62
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25.2%; Pred. No. 0.27;
tive 20; Mismatches 52;
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1.2;
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22 AQNFSRQEVGAATGAVVGGVAGQLFGK--
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-7068
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Best Local Similarity 25.28
Matches 36; Conservative
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Best Local Similarity 27.5$
Matches 25; Conservative
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Patent No. 6551795

GENERAL INFORMATION:

PAPLICATION:

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MICHEL OF OR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-17

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 127
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Factor 10. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26658
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                           24; Indels
      29.7%; Pred. No. 0.14;
                              14; Mismatches
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                                22; Conservative
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89 MGAIAGGTVG 98
      Best Local Similarity
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US-09-252-991A-26658
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US-09-252-991A-28397
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RESULT 15

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Sequence 19, Application US/08556978B

Sequence 19, Application US/08556978B

Sequence 19, Application US/08556978B

GENERAL HIGORANION:
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COMPUTER READABLE FORM:
MCDION TYPE: DELAWARE
TOWNERS: IMM PROCEOUT WINDOWS 95
COMPUTER READABLE FORM:
MCDION TYPE: DELAWARE
TOWNERS: IMM PROCEOUT WINDOWS 95
COMPUTER INVENTION DATA:
TOWNERS IN MICROSOFT WINDOWS 95
COMPUTER INVENTION DATA:
TOWNERS IN MICROSOFT WINDOWS 95
COMPUTER MARKET TOWNERS: US/08/556,978B
FILLING DATE: UNIVER 15, 1933
TOWNERS: FLOOD:
TITLE CAPAULICATION NUMBER: US/08/556,978B
FILLING DATE: UNIVER 15, 1933
TREDERRING-CHOCKET UNBERS: CR. 9389-A
TELECOMMUTICATION INVENTION:
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Sequence 74, App. Sequence 12104, A Sequence 11322, A Sequence 3, Appli

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US-09-815-242-12113
5 US-10-116-76-14378
0 US-09-738-626-5811
2 US/10/244
5 US/10/124
5 US/10/120
2 US-09-976-782-89
2 US-09-976-782-90
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2 US-09-976-782-90
2 US-09-976-782-90
2 US-09-976-782-90
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1 US-09-978-88-68-28

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ALIGNMENTS

Sequence 14378, A Sequence 5811, Ap Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 89, Appli Sequence 90, Appl

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US-10-261-446-2
November 5, 2003, 20:15:12 ; Search time 19.0259 Seconds (without alignments) 1462.395 Million cell updates/sec
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/ cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*
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/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
/ cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*
/ cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*
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/ cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Query
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836
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Perfect score:
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Sequence 2, Application US/10261446
| Publication No. US20030165526A1
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: Kuzyk, Michael A. |
| APPLICANT: Kay, William W. |
| APPLICANT: Ray, William W. |
| APPLICANT: Thornton, Julian C. |
| TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST |
| TITLE OF INVENTION: RICKETTEIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY |
| TITLE OF INVENTION: VACCINES AND ASSOCIATED PREVENTATIVE THERAPY |
| TITLE OF INVENTION NUMBER: US/10/261,446 |
| CURRENT FILING DATE: 2000-09-15 |
| PRIOR FILING DATE: 2000-09-15 |
| PRIOR FILING DATE: 1999-09-17 |
| NUMBER OF SEQ ID NOS: 20 |
| SOOTHWARE: PATENTIN VERSION 3.0 |
| SOOTHWARE: PATENTIN VERSION 3.0 |
| CONTRACT PATENTING DATE: 1099-09-17 |
| SOOTHWARE: PATENTING DATE: DATE SOOTH AND ASSOCIATED AND ASSOCIATED AND ASSOCIATED AND ASSOCIATED AND ASSOCIATED AND ASSOCIATED AND ASSOCIATED AND ASSOCIATED PREVENTATIVE THERAPY STRING PATE: 2000-09-15 |
| NUMBER OF SEQ ID NOS: 20 |
| SOOTHWARE: PATENTING DATE: 1099-09-17 |
| SOOTHWARE: PATENTING DATE: 2000-10 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Piscirickettsia salmonis US-10-261-446-2
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Sequence 2, Appli Sequence 4, Appli Sequence 6, Appli Sequence 169, App Sequence 16, Appli Sequence 5, Appli

Description

Sequence 1, Appli Sequence 1, Appli Sequence 341, App Sequence 19, Appl

836 815 815 128.5 112 83.5 81.5 81.5 80.5 79.5 79.5 77.5 77.7

100.0 97.5 97.5 113.4 10.0 9.7 9.7 9.7

Sequence 101, App Sequence 21, Appl Sequence 1381, Ap Sequence 33055, A Sequence 8774, Ap

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Sequence 16, Application US/10261446
Publication No. US20030165526A1
Publication No. US20030165526A1
Publication No. US20030165526A1
APPLICANT: Ruzyk, Michael A.
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Thornton, Julian C.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
CURRENT APPLICATION NUMBER: US/10/261,446
                                                                                                                                                                                                                                                 157 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 216
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                                                                                                                                                            Gaps
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GENERAL INFORMATION:

APPLICANT: Whiteley, Marvin

APPLICANT: Bangera, M. Gita

APPLICANT: Bangera, M. Gita

APPLICANT: Greenberg, Everett Peter

ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF TITLE OF INVENTION: METHODS AND COMPOSITION FOR THE MODULATION OF FILE REFERENCE: UIZ-070CP

CURRENT APPLICATION NUMBER: US/10/127,032

CURRENT FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: US 60/285,190

PRIOR PRILING DATE: 2001-04-20

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 170

SOFTWARE: FASTESE FOR Windows Version 4.0
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                                                                                                                                                            1; Indels
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                                                                                                     97.5%; Score 815; DB 12;
98.8%; Pred. No. 3.5e-77;
tive 1; Mismatches 1;
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                                                                                                  Query Match
Best Local Similarity 98.8<sup>1</sup>
Matches 158; Conservative
                           (-95) .. (-1)
  NAME/KEY: SIGNAL
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APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Kay, William W.
APPLICANT: Thornton, Juliam W.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
TITLE REPERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US, 10/261,446
CURRENT PILING DATE: 2002-09-30
PRIOR PRIOR APPLICATION NUMBER: US 60/577,374
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Burian, Jan
APPLICANT: Thornton, Juliam W.
APPLICANT: Thornton, Juliam W.
TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE THERAPY
FILE REFERENCE: 4616-64094
CURRENT APPLICATION NUMBER: US 09/677,374
PRIOR PRILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR APPLICATION NUMBER: US 60/154,437
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
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ERROQYCREFQOKAMIAGOKQEIYGTACRQPDGRWQVISTEK 162
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Pred. No. 1.9e-77;
1; Mismatches 1;
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                                                                                                                                                                               ; Sequence 4, Application US/10261446; Publication No. US20030165526A1; GENERAL INFORMATION: APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10261446
Publication No. US20030165526A1
GENERAL INFORMATION:
APPLICANT: Kuzyk, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.8%;
Matches 158; Conservative
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LENGTH: 161
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LENGTH: 256
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US-10-261-446-4
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Publication No. US20030192077A1
GENERAL INFORMATION:
APPLICANT: Yang, Jianjun G.
TITLE OF INVENTION: Production of Silk-Like Proteins in Plants
FILE REPREBUCE: BCIO14 US NA
CURRENT APPLICATION NUMBER: US/10/414,760
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: US/09/863,859
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 651;
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9.7%; Score 81.5; DE
Best Local Similarity 36.8%; Pred. No. 6.7;
Matches 25; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                          6.7;
                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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Pred. No. 6.
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Patent No. US/0020102679A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Boillon, Davin C.
APPLICANT: Secrist, Heather
APPLICANT: Lodes, Michael J.
APPLICANT: Algate, Paul A.
                  PRIOR APPLICATION NUMBER: 09/247,806
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: PR 98/01614
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO I
                                                                                                                                                                                                                                                                                                                                                                          28 QEVGAATGAVVG----GVAGQ-
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  2001-05-22
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 36.8%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 29
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 651
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Nephila clavipes
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US-09-864-864-341
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US-10-414-760-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10091724
; Sequence 5, Application US/20030105310A1
; Publication No. US20030105310A1
; GENERAL INFORMATION:
    APPLICANT: Children's Medical Center Corporation
    APPLICANT: Ashkar. Samy
; TITLE OF INVENTION: Method to Screen Peptide Libraries Using Minicell Display
; TITLE OF INVENTION NUMBER: US/10/091,724
; CURRENT APPLICATION NUMBER: US 60/306,946
; PRIOR APPLICATION NUMBER: US 60/306,946
; PRIOR FILING DATE: 2001-07-20
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 53
; SSQ ID NO 5
; SEQ ID NO 5
; LENGTH: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSNETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/861,597
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                 Query Match
13.4%; Score 112; DB 12;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 20; Conservative 0; Mismatches 0;
                  PRIOR APPLICATION NUMBER: US 09/677,374
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/154,437
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                              TYPE: PRT ORGANISM: Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                        110 PVRIYQRYNKQERRQQYCRE 129
                                                                                                                                                                                                                                                                                                                                                                                                                 1 PVRTYQRYNKQERRQQYCRE 20
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Patent No. US20020064539A1
GENERAL INFORMATION:
APPLICANT: PHILLIPPE, Michel
2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
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65 AVLGGQI 71
FILING DATE:
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                                                                                                                                                SEQ ID NO 16
LENGTH: 20
CURRENT
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APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
Modulate Disorders Related To Nitric Oxide/cGMP-Dependent
Protein Kinase Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 VOAEEMVEFSSGLKGMSLNLEPDNVGVVVFGNDKLIKEGDIVKRTGAIVDVPVGE---EL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --IGQSMDQQDKIKLNQSLEKVKAGQ 93
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                                                                                                                                                    Length 553;
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                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                    DB 12;
                                                                                                                                                                                                                                                                                                                 Query Match
9.5%; Score 79.5; Di
Best Local Similarity 25.3%; Pred. No. 8.7;
Matches 41; Conservative 20; Mismatches
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CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-14
NUMBER: OF SEQ ID NOS: 506
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                6 LOGSSLIIISVFLVGCAQNFSRQEVGAA----
  TITLE OF INVENTION: Modulate Disorders Rel
TITLE OF INVENTION: Protein Kinase Signali
FILE REFERENCE: P-NI 3006
CURRENT APPLICATION NUMBER: US/09/738,630
CURRENT FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 105
SOFWARE: FRAELSEQ for Windows Version 4.0
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Publication No. US20030124128A1
GENERAL INFORMATION:
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Hortobagyi, Gabriel D
Pusztai, Lajos
Meric, Funda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
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Monahan, John
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Wang, Youzhen
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US-09-738-630-101
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 302;
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                                                                           APPLICANT: Carter, Darrick
TITLE OF INVENTION: CAMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
FILE REFERENCE: 210121.523
CURRENT APPLICATION NUMBER: US/09/864,864
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 341
SEQ ID NO 341
LENGTH: 302
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; OTHER INFORMATION: Incyte ID No. US20020160382A1 3040213CD1
US-09-981-353-19
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Publication No. US20030166213A1
GENERAL INFORMATION:
APPLICANT: Greenan, Ralph J.
APPLICANT: Shaw, Paul J.
TITLE OF INVENTION: Mehtods For Identifying Compounds That
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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; Patent No. US20020160382A1
; GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0038 US
CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL PROGram
; SEQ ID NO 19
; LENGTH: 553
; TYBE: PRT
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41.8%; Pred. No. 3.1;
tive 5; Mismatches 26;
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Best Local Similarity 25.3%; Pred. No. 8.7;
Matches 41; Conservative 20; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LQGSSLIIISVFLVGCAQNFSRQEVGAA---
                                Mannion, Jane
Benson, Darin R
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 41.8
Matches 23; Conservative
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US-09-864-864-341
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US-09-981-353-19
                                APPLICANT:
APPLICANT:
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Query Match 9.2%;
Best Local Similarity 23.3%;
Matches 31; Conservative
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    APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-029-386-33055
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LENGTH: 208
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                                                                                                                                                                                                             147 LGRVVDALGNAIDGKGPIGSKTRRRVGLKAPGIIPRISVREPMOTGIKAVDSLVPIGRGO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IOCATION: (562)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        naturally occurring L-amino acids
                                                                                                                                                                                     ----TGAVVGGVAGQLFGKG 49
                                                                                                                                                                                                                                                                    ----IGQSMDQQDKIKLNQSLEKVKAGQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 NFSRQEVGAATGAVVGG--VAGQLFGKGS----GRVAMAIGGAVLGGLIGSKIGQSMDQQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|:
157 EKVTMQNLNDRLASYLDKVRALBESNYELBGKIKEWYEKH-GNSHQGEP-RDYSKYYK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 DKI-----KLNQSLEKVKA-----GQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                           Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.4%; Score 79; DB 10; Length 618;
Best Local Similarity 28.0%; Pred. No. 11;
Matches 33; Conservative 13; Mismatches 46; Indels 26; Gaps
                                                                                                    Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-925-300-1381
US-09-925-300-1381
; Sequence 1381, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TILE REFERENCE: PAIO:
; FILE REFERENCE: PAIO:
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FLING DATE: 2000-03-08
; PRIOR FLING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                             207 ----RELIIGDROTGKTSIAIDTIINOKRFNDGSDEKKKLYC 244
                                                                                                                                                                                                                                                                                                                                                 94 VTRWR-----NPDTG-NSYSVEPVRTYQRYN--KQERRQQYC 127
                                                                                                  Query Match 9.5%; Score 79.5; DB 15; Best Local Similarity 25.3%; Pred. No. 8.7; Matches 41; Conservative 20; Mismatches 54;
                                                                                                                                                                                 6 LQGSSLIIISVFLVGCAQNFSRQEVGAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa equals any of the
                                                                                                                                                                                                                                                                50 SGRVAMAIGGAVLG-GLIGSK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-029-386-33055

; Sequence 33055, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:
                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , US-09-925-300-1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
                                                       US-10-177-293-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1381
LENGTH: 618
LENGTH: 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CITILE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 GGGTGGGGGGTGGGGGGTGGGGGGGGGGGGGTVGLPQGVPGGGQDSTALKQTRRPAR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 VKAGQV-----TRWRNPDTGNSYS-------VEPVRTYQ----- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 GAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 EVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.3%; Score 77.5; DB 12; Length 208; Best Local Similarity 30.8%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 489;
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 AGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.2%; Score 77; DB 323.3%; Pred. No. 14; iive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8774, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8774
```

409 LQAGDLLLLHTDGLVPRRWADPRSSEAESGGGTAAVQRLLDLAPRFDGVRTAQHCVRTVV 468

116 -RYNKQERRQQYC 127 : | | | 469 EEFGETEREDDAC 481

g ò g

Search completed: November 5, 2003, 20:27:19 Job time : 20.0259 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 5, 2003, 20:10:11; Search time 11.4715 Seconds (without alignments) 1358.089 Million cell updates/sec Run on:

Title: Perfect score:

US-09-677-374-2 836 1 MNRGCLQGSSLIIISVFLVG......IYGTACRQPDGRWQVISTEK 162 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|            | Description | rickettsial common | Rickettsial common | Rickettsial common | 17K surface antige | Rickettsial common | 17K antigen precur |        | 17K surface antige | conserved hypothet | outer membrane lip | conserved hypothet | protein | protein [i | lipA protein - Rhi | hypothetical prote | opr    | outer membrane lip | outer  | outer   | outer membrane lip | outer membrane lip | s-react | probable secreted | outer membrane pro | hypothetical prote |        | ğ   | ~    | probable outer mem |
|------------|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|---------|------------|--------------------|--------------------|--------|--------------------|--------|---------|--------------------|--------------------|---------|-------------------|--------------------|--------------------|--------|-----|------|--------------------|
|            | ΩI          | Ġ                  | B33971             | A33971             | G97860             | C33971             | A25972             | D83169 | AI3418             | B83514             | S23787             | B82837             | AD2696  | D97478     | S58234             | G87629             | AF0289 | C64921             | F90922 | B85771  | AI0693             | AG0443             | I64130  | AE0644            | AD3350             | H83636             | D85674 |     | 8    | G91049             |
|            | 8           | ~                  | ~                  | ~                  | ~                  | 7                  | N                  | 7      | N                  | ~                  | ~                  | ~                  | N       | ~          | ~                  | ~                  | ~      | ~                  | ~      | ~       | ~                  | ~                  | ~       | N                 | ~                  | ~                  | ~      | ~   | ~    | 0                  |
|            | Length      |                    | 159                | 159                | 159                | 159                | 159                | 182    | 131                | 154                | 155                | 257                | 142     | 125        | 139                | 232                | 155    | 155                | 155    | 155     | 155                | 155                | 155     | 179               | 232                | 304                | 179    | 179 | 179  | 172                |
| *<br>Query | Match       | 35.4               |                    |                    | 35.0               | 34.0               | 34.0               | 15.4   | 15.0               | 13.9               | 13.6               | 13.4               | 13.3    | •          |                    | 13.2               | 13.0   |                    |        | 12.6    | 12.6               | •                  |         | •                 | 12.2               | ٠                  |        | ٠   | 11.8 | 11.7               |
|            | Score       | 296                | 293                | 293                | 293                | 284.5              | ~                  | 128.5  | 125.5              | 116                | 113.5              | 112                | 111.5   | 111        | 111                | 110.5              | 108.5  | 105.5              | 105.5  | . 105.5 | 105.5              | 104                | 102     | 102               | 0                  | 101.5              | 66     | 66  | 66   | 98                 |
| Result     | No.         | -                  | 8                  | e                  | 4                  | S                  | 9                  | 7      | 89                 | σ                  | 10                 | 11                 | 12      | 13         | 14                 | 15                 | 16     | 17                 | 18     | 19      | 20                 | 21                 | 22      | 23                | 24                 | 25                 | 56     | 27  |      | 29                 |

RESULT 2 B33971 Rickettsial common antigen precursor - Rickettsia conorii

| probable outer mem | hypothetical prote | probable exported | probable lipoprote | hypothetical prote | hypothetical prote | glycine-rich prote | hypothetical prote | hypothetical prote | conserved hypothet | keratin, 54K type | PBSX prophage ORF | porin [imported] - | probable outer mem | probable tape meas | hypothetical prote |
|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| D85894             | H65026             | AC0198            | C82230             | AB3091             | H98195             | T05442             | F87413             | G97672             | AE2897             | KRBOVI            | F69732            | AI2910             | G97685             | F91251             | B82998             |
| ~                  | N                  | N                 | 0                  | 7                  | ~                  | ~                  | 0                  | ~                  | N                  | -                 | ~                 | ~                  | 7                  | 7                  | 0                  |
| 172                | 172                | 179               | 223                | 278                | 278                | 608                | 257                | 100                | 100                | 526               | 1332              | 220                | 220                | 691                | 137                |
| 11.7               | 11.7               | 11.7              | 11.5               | 11.2               | 11.2               | 11.2               | 11.2               | 11.0               | 11.0               | 10.8              | 10.8              | 10.7               | 10.7               | 10.7               | 10.6               |
|                    |                    | 8                 | 9                  | 4                  | 94                 | 94                 | .5                 | 92                 | 92                 | 90                | 90                | ī.                 | 89.5               | ī.                 | 83                 |
| 98                 | 98                 | σ                 | ס                  | Ο,                 | •                  |                    | 93                 |                    |                    |                   |                   | 8                  | 83                 | 89                 |                    |

## ALIGNMENTS

| RESULT         | 11.11   |
|----------------|---|
| D33971         |   |
| ric            | rickettsial common antigen precursor - Rickettsia prowazekii  |
| A.N            | N;Alternate names: 17kD surface antigen; outer membrane protein (omp); RP833  |
| C,S            | C; Species: Rickettsia prowazekii   |
| Ď,             | C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 03-Nov-2000   |
| Y.             | C;Accession: D339/1; B11645   |
| ¥: *           | K;Anderson, b.b.; Izlanadow, 1.<br>T processed 1771 Elgo.E201   |
| · E            | ). nacceilo: .i.i, 313-3141, 1503.<br>8.Tile: Comparative sequence analysis of a genus-common rickettsial antigen gene. |
| A; R           | PMID:2768201  |
| A; A           | A; Accession: D33971  |
| A;S            | A;Status: preliminary   |
| A; W           | A; Molecule type: DNA   |
| A;R            | A;Residues: 1-159 <and></and>   |
| O A            | A)(TCOSS-references: GB:M28402; NID:6152461)  |
| R.A.           | J.O.; Sicheritz-Ponten, T.: 7   |
| Nati           | Nature 396, 133-140, 1998   |
| A,T            | A, Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.                                  |
| A; K           | eference number: A71630; MUID:99039499; PMID:9823893  |
| A; A           | A; Accession: B71645  |
| A;S            | A;Status: nucleic acid sequence not shown; translation not shown  |
| A; W           | A; Molecule type: DNA   |
| A; K           | A;Residues: 1-159 <an2></an2>   |
| A;C            |   |
| A C            | A;Experimental source: strain Madrid E  |
| 50             | Cydenetics:   |
| ⊉ (S<br>C)     | A;ene: omp; krass<br>C;Superfamily: rickettsial common antigen  |
| C;K            | C, Keywords: surface antigen  |
| ð              | Onerv Match 35.4%; Score 296; DB 2; Length 159;   |
| ďΩŽ            | Similarity 38.1%; Pred. No. 6.6e-19;<br>1; Conservative 30; Mismatches 55;  |
| Ś              | 9 SSLIIISVFLVGCAONFSROEVGAATGAVVGGVAGOLFGKGSGRVAMAIGGAVLG 63  |
| ÿ              |   |
| q              | 5 SKIMÍTALAASMLQAČNGQSGMNKQGTGTLLGGAAGGALLGSQFGQGKGQLVGVGVGALLG 64  |
| ò              | 64 GLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRXNK 119   |
| q              | 65 AVLGGQIGASMDEQDRRLLELTSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY 119  |
| 8              | 120 OERROOYCREFOOKAMIAGOKOBIYGTACROPDGRWOVIS 159  |
| 7              |   |
| q <sub>0</sub> | 120 RNSAGGYCREYTQTVIIGGKQQKTYGNACRQPDGQWQVVN 159  |

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142 EIYGTACROPDGRWOVIS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: C33971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: C33971
                                                                                                                                                                                                                                                                                                         61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rickettsia rickettsii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C;Date: 17-11, 1990 #sequence_revision 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen
C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: G97860
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
                 CjDate: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
CjAccession: B3371
RjAnderson, B.B.; Tzianabos, T.
RjAnderson, B.B.; Tzianabos, T.
A.Bacteriol. 171, 5199-5201, 1989
A.Title: Comparative sequence analysis of a genus-common rickettsial antigen gene. A;Reference number: A3371; MUID:89359171; PMID:2768201
A,Reference preliminary
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-159 <AND>
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17K surface antigen precursor [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep_2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                               4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLIGSKIGOSMDOODK----IKLNQSLEKVKAGQVTRWRNPDIGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsial common antigen precursor - Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKIMIİALATSMLQACNGPGGMNKQGTGTLLGGAGGGALLGSQFGKGKGQLVGVGVGALLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
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                                                                                                                                                                                                                                                                                                                                                                                                                              9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
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                                                                                                                                                                                                                                                                                                                                                                               14; Gaps
                                                                                                                                                                                                                                                       A,Cross-references: GB:M28479; NID:g152463; PIDN:AAA26379.1; PID:g152464 C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OERROOYCREFOOKAMIAGOKOEIYGTACROPDGRWOVIS 159
                                                                                                                                                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                                                                                                             Match 35.0%; Score 293; DB 2; Local Similarity 38.1%; Pred. No. 1.2e-18; les 61; Conservative 29; Mismatches 56
Species: Rickettsia conorii
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C;Species: Rickettsia rickettsii
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 20-Aug-1999
C;Accession: A2597
C;Accession: A2597
B;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabos, T.; McDade, J.E.; Fu, Z.Y.; E
B;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabos, T.; McDade, J.E.; Fu, Z.Y.; E
J. Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia rickettsii
A;Reference number: A25972; MuID:87222152; PMID:3108232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R,Anderson, B.E.; Tzianabos, T.
V. Bacteriol. 171, 5199-5201, 1989
A,Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A,Reference number: A33971; MUID:89359171; PMID:2768201
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893 A;Accession: G97860 A;Atcession: G97860 A;Atcus: preliminary A;Molecule type: DNA A;Residues: 1-159 <KUR> A;Coss-references: GB:AE006914; PIDN:AAL03825.1; PID:g15620425; GSPDB:GN00173 C;Genetics: A;Gene : omp C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 INQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYORYNKQERROQYCREFOOKAMIAGOKQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rickettsia typhi
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 SRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK
                                                                                                                                                                                                                                                                                                                                                                                                                              9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 QERROQYCREFOQKAMIAGQKQEIYGTACROPDGRWQVIS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsial common antigen precursor - Rickettsia typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 284.5; DB 2
Pred. No. 6.8e-18;
                                                                                                                                                                                                                                                                                               Score 293; DB 2;
Pred. No. 1.2e-18;
                                                                                                                                                                                                                                                                              35.0%; Scott No. 1.38.1%; Pred. No. 1.1.
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34.0%; Score 284.5; I
Best Local Similarity 39.9%; Pred. No. 6.8e
Matches 55; Conservative 25; Mismatches
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C;Accession: B83514
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathera; A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-154 <STO>
A;Cross-references: GB:AE004537; GB:AE004091; NID:g9946960; PIDN:AAG04442.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outer membrane lipoprotein precursor - YerBinia enterocolitica
C;Species: YerBinia enterocolitica
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 29-Sep-1999
C;Accession: 22.787
C;Accession: 22.787
M;Bacumler, A.J.; Hantke, K.
J. Bacteriol. 174, 1029-1035, 1992
A;Atitle: A lipoprotein of YerBinia enterocolitica facilitates ferrioxamine uptake in Bs<sup>r</sup> A;Reference number: 823786; MUID:92121089; PMID:1732192
A;Accession: 823787
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                   152
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                                                                                                                                                                                                                                                                                                            71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 GKGSG--FPSLGGSSQKPETNLLASLGNGLFGNSASQLSAADRRKALEAEYRALEYSPAG
                                                                                                                                                                                                                                                                                                                                                                   93 QVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGTACRQPD
                                                                                                                                                                                                                                                           47 GKGSGRVAMAIGG------AVLG-GLIGSKIGQ--SMDQQDKIKLN-QSLEKVKAG
                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                 23;
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                                                                                                                                             Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 13.9%; Score 116; DB 2; Length 154; Local Similarity 25.0%; Pred. No. 0.0042; les 34; Conservative 21; Mismatches 41; Indels 4
                                                                                                                                                                                                 Indels
                                                                                                                                       ; Score 125.5; DB 2;
; Pred. No. 0.00052;
18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNRGCLQGSSLIIISVFLVGC----AQNFSRQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: PA1053
C;Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :::| ||: |
121 STRAYVQQVDQGQIFR 136
A; Experimental source: strain 16M C; Genetics: A; Gene: BME11335 A; Map position: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --NOSLEKVKAGQVTR 96
                                                                                                                                          Query Match
Best Local Similarity 31.7%;
Matches 39; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 GRW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 GSW 127
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Best Local S:
Matches 34
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S23787
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C; Date: 15.Sep-2000 #sequence_revision 15.Sep-2000 #text_change 01-Mar-2002
C;Accession: D83169
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A62950; MUID:20437337; PMID:10984043
A;Reference number: A62950; MUID:20437337; PMID:10984043
A;Residues: 1-182 <STO>
A;Cossion: DFIIMINARY
A;Molecule type: DNA
A;Residues: 1-182 <STO>
A;Cross-references: GB:AE004799; GB:AE004091; NID:g9949981; PIDN:AAG07206.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3819
C;Superfamily: PAL cross-reacting lipoprotein
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, i. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Pseudomonas aeruginosa (strain PAO1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: AE008917; PIDN: AAL52516.1; PID: 917983328; GSPDB: GN00190
                                                                                                                                                                                                                                                                                                                                                                         64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
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                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein PA3819 [imported] - Pseudomonas aeruginosa (E
C;Specise: Pseudomonas aeruginosa
C;Date: 15-Sep.2000 #sequence_revision 15-Sep-2000 #text_change 01-Mar-2002
C;Accession: D83169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17K surface antigen precursor [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                           9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
                                                                                                                                                                                                                                                                                              28 QEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKI-----
                                                                                                                                          Query Match 34.0%; Score 284; DB 2; Length 159;
Best Local Similarity 37.5%; Pred. No. 7.5e-18;
Matches 60; Conservative 29; Mismatches 57; Indels 14; Gaps
                                  A,Residues: 1-159 <AND>
A,Cross-references: GB:M16486; NID:g152467; PIDN:AAA26381.1; PID:g152468
C,Superfamily: rickettsial common antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 RNSTGQYCREYTQTVVIGGKQQKAYGDACRQPDEQWQVVN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KAGQVTRWRNP 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
Les 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-131 <KUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: AI3418
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Matches
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<u>ب</u>

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LipA protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: D97478
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman
A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
                                   Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                         ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                       A;Residues: 1142 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41986.1; PID:g17739358; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 LEKVKAGQVTRWRNPDT-GNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 IGOSMDQQDKIKL----NQSLEKVKAGQVTRWRNPDT-GNSYSVEPVRTYQRYNKQERRQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AE007869; PIDN: AAK86781.1; PID: g15155981; GSPDB: GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 SILCVSM-LSAC-----TITGTRPAG--GSLFGR-SAQPSTPFLANLQGGIVG-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LSACTITGIRPAGGSLFGR-SAQPSIPFLANLQGGIVG-KSGVELDRGDQIKALEAESYKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 VGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL----NQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 SLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
13.3%; Score 111.5; DB 2;
Best Local Similarity 27.2%; Pred. No. 0.0095;
Matches 41; Conservative 21; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 27.5%; Pred. No. 0.0092;
Matches 36; Conservative 18; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 ONCROYSHTLTVDGRDTRVRGAACRNDDGSW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OYCREFOOKAMIAGOKQEIYGTACROPDGRW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
S58234
lipA protein - Rhizobium leguminosarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                C'Genetics:
A;Gene: lipA
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: AGR C 1782
A;Map position: circular chromosome
P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 GTACROPDGRW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAACRNDDGSW 121
                                                                                                                                                                                                                         A;Accession: AD2696
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: B82837
R,anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: for a complete list of authors see reference number A59328 below
A; Accession: B82837
A; Accession: B82837
A; Molecule type: DNA
A; Residues: 1-257 <SIM>A; Residues: 1-257 <SIM>A; Cross-references: GB: AE003872; GB: AE003849; NID: g9104975; PIDN: AAF82991.1; GSPDB: GN001
A; Experimental source: strain 9a5c
B; Simpson, A.J.G; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A'Experimental source: strain 93.5

A'Experimental source: strain 93.5

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H as Neto, B.; Docena, C.; Bl-Dorry, H.F. Facincani, A.P.; Ferrira, A.J.S.

Bubmitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fronco, M.C.; Fronco, M.D.; Jungueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, B.E.; Laign chado, M.A.; Madeira, A.M.B.N.; Matsukuma, A.Y.; Marino, C.L.; Marques, M.V.; Martins, E.A;Authors: Martins, B.M.F.; Matsukuma, A.Y.; Marino, C.L.; Marques, M.V.; Martins, F. G.; Nunes, L.R.; Oliveira, M.A.; Meolira, M.C.; de Oliveira, R.C.; Palmieri, D.P.; Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.; Aluthors and Silva, A.C.R.; da Silva, A.M.; Sawasak

A;Ruthors and Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr.; W.A.; da Silvaineri, A.R.; Tanhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zawasak

A;Reference number: ASS9128
                                                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                                                                                                                                                                                7 AVAIAAVTLTGCANNNTLSGDVFSASQAKQVQTVTYGTLLSVRPVTIQGGDDNNVMGAIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein XF0178 [imported] - Xylella fastidiosa (strai
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lipA protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                    51; Gaps
                                                                         A;Cross-references: EMBL:X60448; NID:948577; PIDN:CAA42977.1; PID:948579
C;Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                      Length 155;
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                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                          DB 2;
                                                                                                                                                                                   Query Match
Best Local Similarity 24.7%; Pred. No. 0.007;
Matches 37; Conservative 19; Mismatches
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Pred. No. 0.016;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --NQSLEKVKAGQVTRWRNPDTGNSYSVEP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 VQKQGPTRFSVGQ--RVMLASSGSTVTVSP 154
                                                                                                                                                                                                                                                                                                                                          10 SLIIISVFLVGCAQN-----FSRQE---
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Best Local Similarity 50.0%;
Matches 20; Conservative
                                      1-155 <BAE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
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                                      A; Residues:
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hypothetical protein CC3073 [imported] - Caulobacter crescentus
G;Species: Caulobacter crescentus
G;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
G;Accession: 687201
B; Accession: 687201
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ernolaeve, M.; Wilte, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 99, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-232 <STO>
A;Conetics:
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C;Species: Rhizobium leguminosarum
C;Date: 13-40a-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
C;Accession: S58234
R;Yeoman, K.H.; Delgado, M.J.; Downie, J.A.; Johnston, A.W.B.
R;Yeoman, K.H.; Delgado, M.J.; Downie, J.A.; Johnston, A.W.B.
R;Yeoman, K.H.; Delgado, M.J.; Downie, J.A.; Johnston, A.W.B.
R;Yeoman, K.H.; Delgado, M.J.; Downie, J.A.; Johnston, A.W.B.
A;Reference number: SS823
A;Recession: S5823
A;Accession: S5823
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Best Local Similarity 25.2%; Pred. No. 0.01;
Matches 38; Conservative 18; Mismatches 65; Indels 30; Gaps
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26.9%; Pred. No. 0.02;
ive 22; Mismatches 56; Indels 39; Gaps
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plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Madrid E;
MEDLINE=89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
"Comparative sequence analysis of a genus-common rickettsial antigen gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99039499; PubWed=9823893; Andersson J.O., Andersson S.G.E., Zomorodipour A., Andersson J.O., Andersson S.G.E., Zomorodipour A., Andersson J.O., Exiestiz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; The genome sequence of Rickettsia prowazekii and the origin of mitoofondrian.; Nature 396:133-140(1998).

Nature 396:133-140(1998).

-i- SUBCELJULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; MZ6482; AAA26778.1; ALT_SEQ.
EMBL; AJ235273; CAA15258.1; -
PRS; D33971; D33971.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.
SIGNAL
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                     P15999 r
P25705 H
P194843 H
P194843 H
P18538 d
P18538 d
P18595 d
P14593 H
P12405 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsia prowazekii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
  P19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.4%; Score 296; DB 1; Length 159; 38.1%; Pred. No. 1.5e-18; Live 30; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 159 17 kDa SURFACE ANTIGEN.
20 20 N-ACYL DIGLYCERIDE (PROBABLE)
159 AA; 16672 MW; A33D404B65EEB071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    159 AA
                                                                                                                                                                                                                                                                                           ALIGNMENTS
                     ATPA_RAT
ATPA_HUMAN
KICJ_HUMAN
ATPO_BOVIN
ATPA_MOUSE
VIAB_ECOLI
YIAD_ECOLI
VIAB_ECOLI
CANS_MOUSE
CSP_FIAMA
ATPA_ANASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 171:5199-5201(1989)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-R.rickettsii,
MEDLINE-87222152; PubMed-3108232;
Anderson B.E., Regnery R.L., Carlone G.M., Tzianabos T., McDade J.E.,
Fu Z.Y., Bellini W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative sequence analysis of a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 170:4493-4500(1988).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-30 FROM N.A.
SPECIES=R.rickettsii;
MEDLINE=89008059; PubMed=3139629;
Anderson B.E., Baumstark B.R., Bellini W.J.;
"Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii; transcription and posttranslational modification."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21442074; PubMed=11557893; Ogata H., Audic S., Renesto-15Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                   Rickettsiaceae; Rickettsia; Alphaproteobacteria; Rickettsiales;
NCBI_TaxID=781, 783;
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N-ACYL DIGLYCERIDE (PROBABLE)
N -> D (IN REF. 3).
                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                               SPECIES=R.conorii, and R.rickettsii;
MEDLINE=89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIES=R.conorii, STRAIN=Malish 7;
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EMBL; M26480; AAA26376.1; -.
EMBL; AE008675; AAL03825.1; -.
EMBL; M16486; AAA26381.1; -.
EMBL; J03371; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rickettsii.";
J. Bacteriol. 169:2385-2390(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 171:5199-5201(1989)
                                                                                                        17 kDa surface antigen precursor.
OMP OR RC1287.
                      01-NOV-1988 (Rel. 09, Created)
01-AUG-1990 (Rel. 15, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                             Rickettsia conorii, and
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PIR; A31836; A31836
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SEQUENCE FROM N.A.
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146
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                                                                                                                                          65 AVLGGQIGASMDEQDRRLIELTSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY---- 119
                                                                                                             GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
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  63
                                                     SKIMIIALAASMIQACNGQSGMNKQGTGTLLGGAGGALLGSQFGQGKGQLVGVGVGALLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
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  SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
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-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=YH;
BULINE-529950; PubMed=7714214;
Furuya Y., Katayama T., Yoshida Y., Kaiho I.;
Fyecific amplification of Rickettsia japonica DNA from clinical apecinens by PCR.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
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Rickettsiaceae; Rickettsiaae; Rickettsia.
NCBI TaxID=35790;
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17 KDB SURRADE ANTIGEN.
17 ACYL DIGLYCERIDE (PROBBLE)
7 CDDCE7CEBDCD6841 CRC64;
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                                                                                                                                                                                                                   120 QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVIS 159
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
17 kDa surface antigen precursor.
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Best Local Similarity
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17KD_RICCN
ID 17KD_RICCN
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Q52764;
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159 AA.

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142 TTYGNACRQPDGQWQVVN 159
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                                                                                                                                   17KD RICAU
P50928;
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SEQUENCE
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                                                                                                                                                                                                                                                                      65 AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 LNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ 141
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                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-8935917; PubMed=2768201;
Anderson B.E., Tzianabos T.;
"Comparative sequence analysis of a genus-common rickettsial antigen
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Rickettsiaceae, Rickettsieae, Rickettsia.
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                                                                                                            Indels
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                    206A2BBF74FCE169 CRC64;
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20 20 N-ACYL DIGLYCERIDE (PROBAI
159 AA; 16549 MW; 08973E2648FD8CD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                           120 RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
                                                                                                                                                                                                                                                                                                                                    120 OERROOYCREFOOKAMIAGOKOEIYGTACROPDGRWQVIS 159
                                                                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.0%; Score 284.5; DB 1; 39.9%; Pred. No. 1.4e-17; ive 25; Mismatches 49;
                                                                35.0%; Score 293; DB 1;
38.1%; Pred. No. 2.7e-18;
iive 29; Mismatches 56
  G -> E (IN REF. 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 AA
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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                    16581 MW;
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                                                                                     Best Local Similarity 38.1
Matches 61; Conservative
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nes 55; Conservative
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                    159 AA;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                               Baird R.W., Ross B., Dwyer B.;
Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
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PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
OUTER membrane; Lipoprotein; Antigen; Signal.
SIGNAL 1 19 BY SIMILARITY.
CHAIN 20 >154 17 KDA SURFACE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 276; DB 1; Length 154;
Pred. No. 7.4e-17;
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                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
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38.1%; Pred. No. /...
''ve 27; Mismatches
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                                Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C., Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
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Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35792;
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Outer membrane; Lipoprotein; Antigen; Signal.
SIGNAL 1 19 BY SIMILARITY.
CHAIN 20 >154 IY Aba SURRACE ANTIGEN.
LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 20 N-ACYL DIGLYCERIDE (PROBAL 154 154 159 MW; B4FBE4C29D943581 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
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PROSTIE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal.
STGNAL.
19 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U11013; AAB07704.1; -.
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nes 57; Conservative
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STRAIN=MO 85-1084;
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                                                                                                                                                                                                                                                                                                                                                                                                                           65 AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---- 119
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                                                                                                                                                                                                                                                                                         9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
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                                                                                                                                                                                               57; Indels 14;
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Rickettsiaceae; Rickettsieae; Rickettsia.
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SIGNAL 1 19 BY SINTLARITY.
10 > 154 17 kba SURACE ANTIGEN.
LIPID 20 > 154 N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                           Length 154;
  17 kDa SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Indels
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20 20 N-ACYL DIGLYCERIDE (PROBAL
154 154 NW, OCF85AD5D96DFEFB CRC64;
20 >154 17 KDa SUKFACE ANALLELING PROBAL 20 20 N-ACYL DIGLYCERIDE (PROBAL 154 154 AA; 15897 MW; SD06F45F9DBD5EEC CRC64;
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                                                                                                                                        ; Score 261; DB 1;
; Pred. No. 1.4e-15;
28; Mismatches 57,
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
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                                                                                                                                           31.2%;
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es 56; Conservative
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MEDLINE=92108069; PubMed=1729713;
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                                                                                                                                                                                                                    Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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EMBL; U11017; AAB07705.1; -.

EMBL; U11017; AAB07705.1; -.

PROSITE; PSO0013; PROKAR LIPOPROTEIN; 1.

PROSITE; PSO0013; PROKAR LIPOPROTEIN; 1.

SIGNAL 1 19 BY SIMILARITY.

1 19 17 kDa SURFACE ANTIGEN.

1 ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.9%; Score 258; DB 1; Length 15
36.1%; Pred. No. 2.5e-15;
ive 28; Mismatches 57; Indels
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120 RNSTGQYCREYTQTVVIGGKQQKAYGNACLQPDGQ 154
                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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                                                       STANDARD;
                                                                                                                                                                                                                                                       anchor (Probable).
                                                                                                                                                                                                           STRAIN=Ohio 83-441;
                                                                                                                                      Rickettsia montana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                        NCBI_TaxID=33991;
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                                                      17KD RICMO
P50929;
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17KD_RICCA
ID 17KD_R
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by a lipid
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STRAIN=ATCC 51872 / WA-C / Serotype O:8;
STRAIN=ATCC 51872 / WA-C / Serotype O:8;
STRAIN=ATCC 51872 / WA-C / Serotype O:8;
Bacumler A.J., Hantke W.G.,
"A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine uptake in Escherichia coli.";
"Bacteriol. 174-11029-1035 (1992).
-1- FUNCTION: FACILITATES FERRIOXAMINE UPTAKE.
-1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 AA; 8372 MW; AD289A48EAB19E0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, M82879; -; NOT ANNOTATED CDS.
InterPro; IPR000437; Prok lipoprot.
PROSITE; PS00013; PROKAR LIPOPROTEIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 37, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 NPDTGNSYSVEPVRTYQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 26, Created)
(Rel. 26, Last seq
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NCBI_TaxID=630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yersinia enterocolitica
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Res. 3:363-377(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96133688; PubMed=8544813;
Ludwig A., Tengel C., Bauer S., Bubert A., Benz R., Mollenkopf H.-J.,
Goebel W.;
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "SlyA, a regulatory protein from Salmonella typhimurium, induces haemolytic and pore-forming protein in Escherichia coli."; Mol. Gen. Genet. 249:474-486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Aiba H., Rasai H., Kashimoto K., Kimura S., Kitekawa M.,
Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Yamamoto Y., Horiuchi T.;
A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                     51;
                                                                                                                                                                                                          35 GAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL----
     EMBL; Xousso, 23787.
PIR, S23787; S23787.
PROSITE; PSOROU13; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal.
SIGNAL 1 17 OUTER MEMBRANE LIPOPROTEIN PCP.
CHAIN 18 155 OUTER MEMBRANE LIPOPROTEIN PCP.
18 N-ACYL DIGLYCERIDE (POTENTIAL).
                                                                                                             DB 1; Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                     Indels
                                                                                                                                  43;
                                                                                                            13.6%; Score 113.5; DB : 24.7%; Pred. No. 0.0053;
                                                                                                                                                                                                                                                                                                                                                    P55741; P76183;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
older membrane lipoprotein slyB precursor.
SLYB OR B1641 OR Z2655 OR ECS2350 OR SF1668.
                                                                                                                                                                                                                                                         --NQSLEKVKAGQVTRWRNPDTGNSYSVEP 110
                                                                                                                                                                                                                                                                        127 VQKQGPTRFSVGQ--RVMLASSGSTVTVSP 154
                                                                                                                                                                                                                                                                                                                                            155 AA
                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli,
Escherichia coli 0157:H7, and
  EMBL; X60448; CAA42977.1; -.
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                                                                                                          Ouery Match
Best Local Similarity 24.7'
Matches 37, Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=E.coli; STRAIN=0157.H7 / RIMD 0509952;
MEDLINE=21156211; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hatcori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 MVGLSLVGCVNNDTLSGDVYTASEAKQVQNVSYGTIVNVRPVQIQGGDDSNVIGAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).

- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                   Perna N.T., Plunkett G. III. Burland V., Mau B., Glasner J.D., Rose D.J., Maylew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
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ECGENE; EG13409; S1yB.

ECGENE; EG13409; S1yB.

DROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

OUTER membrane; Lipoprotein; Signal; Complete proteome.

SIGNAL 1 17

CHAIN 18 155 OUTER MEMBRANE LIPOPROTEIN SLYB.

CHAIN 18 18 N-ACYL DIGLYCERIDE.

TT TIN REF. 2).

TT TIN REF. 2).
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-!- SIMILARITY: TO S.TYPHIMURIUM SLYB, H.INFLUENZAE PCP AND
Y.ENTEROCOLITICA PCP.
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SEQUENCE FROM N.A.
SPECIES-E.coli; STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
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Best Local Similarity
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Best Local Similarity
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P10325;
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            VGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRW 97
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MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES S. Typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINB=21534948; PubMed=11677609; MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Floraed L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; Complete genome sequence of Salmonella enterica serovar Typhimurium
                            -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Potential).
-!- SIMILARITY: TO E.COLI SLYB, H.INFLUENZAE PCP AND Y.ENTEROCOLITICA
                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.typhimurium;
MEDLINE=96133688; PubMed=8544813;
Ludwig A., Tengel C., Bauer S., Bubert A., Benz R., Mollenkopf H.-J.,
Goebel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain C. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davis R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica servoar Typhi CT18."
                                                                                                                                                                                                                                                                                                                                                                                                             "SlyA, a regulatory protein from Salmonella typhimurium, induces haemolytic and pore-forming protein in Escherichia coli."; Mol. Gen. Genet. 249:474-486(1995).
                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
14-cr membrane lipoprocein slyB precursor.
15-SEP-2004 (STM1445 OR STY1677 OR T1313.
                                                                 98 RNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                           --- DDGNTIMVVQKQGNTRFSPGQR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
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                                                                                                                                                                                                                                                                                                     Enterobacteriaceae; Salmonella
NCBI_TaxID=602, 601;
                                                                                                                                                                                         (Rel. 35, Created)
                                                                                                                                                                                                                                                        Salmonella typhimurium, and Salmonella typhi.
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                                                                                                                                                              STANDARD;
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Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;
"Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lippotcein and an antigenically related 15,000-dalton protein from Haemophilus influenzae.";
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STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MELSINE=95350630; PubMed=7542800;
Rerlachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last annotation update)
04-FEB-2003 (Rel. 41, Last annotation update)
04-cremenane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL cross-reacting lipoprotein).
PCP OR LPP OR HI1579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane; Lipoprotéin; Signal; Complete proteome.
SIGNAL 1 17 POTENTIAL.
CHAIN 18 155 OUTER MEMBRANE LIPOPROTEIN SLYB.
LIPID 18 18 N-ACYL DIGLYCERIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.6%; Score 105.5; DB 1; Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105.5,
Pred. No. 0.025;
Pred. no. 10618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 AA; 15548 MW; 82FDDCDCBABD55A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Mismatches
                                                                                                                                                                                                                                                                                                   EMBL; S80790; AAB35871.2; -.
EMBL; AE008762; AAL20367.1; -.
EMBL; AL627271; CAD01922.1; -.
EMBL; AL627371; CAD01922.1; -.
STYGENE; SG16539; ABYB.
PROSITE; PS00013; PROKAR_LIPORROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | : :|
123 TIMVVOKOGNTRFSAGOR 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Conservative
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SEQUENCE
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                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the butopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
"Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SPECIES=E.coli; STRAIN=K12;

MEDLINE=97061202; PubMed=8905121;

MEDLINE=97061202; PubMed=8905121;

Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,

Ikemoto K., Inda T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,

Mori H., Mortomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,

Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

Yano M., Horiuchi T.;

"A 718-kb DNA sequence of the Escherichia coli K-12 genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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SPECISESE.COL1; STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Greeger J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                   to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 VGAATGAVVGGVAGOLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
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0
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CSLVAEFVF -> VAGRRVRI (IN REF. 1).
D7880327FCF0C985 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OUTER MEMBRANE LIPOPROTEIN PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2%; Score 102; DB 1; Length 155; 39.6%; Pred. No. 0.051; ive 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                             -!- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLYB AND TO
                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; H11579; -.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YCFJ ECOLI STANDARD; PRT; 179 AA. P37756; P75951; 01-0CT-1994 (Rel. 30, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein ycfJ. YCFJ OR B1110 OR C1383 OR SF1114.
                                                                   -! - SUBCELLULAR LOCATION: Attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 623;
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EMBL; U32832; AAC23228.1; -.
PIR; I64130; I64130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Conservative
                                                                                                                                       Y.ENTEROCOLITICA PCP.
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Escherichia coli 06, and
                                              Science 269:496-512(1995)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Matches
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YCFJ_ECOLI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-63 FROM N.A.
SPECIES=E.coli; STRAIN=K12;
MEDLINE=81236546; PubMed=6265208;
Young J.G., Rogers B.L., Campbell H.D., Jaworowski A., Shaw D.C.;
"Nucleotide sequence coding for the respiratory NADH dehydrogenase of Escherichia coli. UUG initiation codon.";
Eur. J. Biochem. 116:165-170 (1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                           SEQUENCE FROM N.A.
SPECIES=E.coli, STRAIN=06;H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
MayNew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.flexmeri; STRAIN=301 / Serotype 2a,
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang C., Yuang X., Zhang J., Yang G., Wu H., Qu D., Dong Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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corresponding to the 12.7-28.0 min region on the linkage map.", DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 GSVLGAVAGGVIGHQFGGGRGKDVATVVGALGGGYAGNQÍQGSLQESD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borodovsky M., Rudd K.E., Koonin E.V.; "Intrinsic and extrinsic approaches for detecting genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.8%; Score 99; DB 1; Length 179; 27.1%; Pred. No. 0.11;
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EMBL, VO0306; -; NOT ANNOTATED CDS.
EMBL, AE015138; AAN42732.1; ALT_INIT.
PIR; C64855; C64855.
ECGGent: E012444; ycfJ.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSWEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial genome.";
Nucleic Acids Res. 22:4756-4767(1994).
-!- SIMILARITY: TO RICKETTSIA 17 kDa SURFACE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 AGQVIRWRNPDIGNSYSVEPVRIYORYNKQERRQQY 126
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MEDLINE=95075659; PubMed=7984428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000211; AAC74194.1; -. EMBL; D90746; BAA35925.1; -.
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Search completed: November 5, 2003, 20:13:25 Job time: 7.43523 secs

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November 5, 2003, 20:09:46; Search time 23.7824 Seconds (without alignments) 1757.794 Million cell updates/sec
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1 MNRGCLQGSSLIIISVFLVG.....IXGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                 830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
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sp_archeap:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                             sp.human:*
sp.invertebrate:*
sp.mammal:*
sp.mhc:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                             SPTREMBL 23:*
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Perfect score:
                                                                                                                                                                                             Scoring table:
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                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|        |       |       |                 |    | SUMMAKIES |                    |
|--------|-------|-------|-----------------|----|-----------|--------------------|
| Result |       | ouerv |                 |    |           |                    |
| No.    | Score | Match | Match Length DB | DB | ΩI        | Description        |
| -1     | 836   | 100.0 | 162             | ~  | Q9F9K8    | Q9f9k8 pisciricket |
| 7      | 313.5 | 37.5  | 148             | N  | 054381    | 054381 rickettsia  |
| e      | 291   | 34.8  | 159             | ~  | Q9F9F2    | Q9f9f2 rickettsia  |
| 4      | 266.5 | 31.9  | 137             | ~  | 052252    | O52252 rickettsia  |
| ស      | 260.5 | 31.2  | 144             | ~  | Q9K2N6    | Q9k2n6 male-killin |
| 9      | 259.5 | 31.0  | 137             | 7  | 031065    | O31065 rickettsia  |
| 7      | 259.5 | 31.0  | 144             | ~  | Q9K4W8    | Q9k4w8 male-killin |
| 60     | 252   | 30.1  | 154             | 7  | 053154    |                    |
| თ      | 247   | 29.5  | 151             | ~  | Q9F9Q9    | Q9f9q9 rickettsia  |
| 10     | 242.5 | 29.0  | 131             | ~  | Q8KLT4    | Q8klt4 rickettsia  |
| 11     | 242.5 | 29.0  | 131             | 7  | Q8KLT5    | Q8klt5 rickettsia  |
| 12     | 237.5 | 28.4  | 131             | 7  | Q9F0Q1    | Q9f0q1 rickettsia  |
| 13     | 237.5 | 28.4  | 131             | 7  | 052637    | Q52637 rickettsia  |
| 14     | 236.5 | 28.3  | 131             | ~  | Q8KLU2    | Q8klu2 rickettsia  |
| 15     | 236.5 | 28.3  | 131             | 7  | Q9L522    | Q91522 rickettsia  |
| 16     | 223.5 | 26.7  | 105             | ~  | 031208    | 031208 rickettsia  |

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1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGCVAGQLFGKGSGRVAMAIGGA 60

1 MNRGCLOGSSLIIISVFLVGCAQNFSRQBVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA

| Q98594 rhizobium 1 Q9agc7 rickettsia Q8atu7 brucella ab 0,82x89 rhizobium m Q9hxi3 pseudomonas Q8y27 brucella ab 0,91481 pseudomonas Q8y27 brucella fas 0,8427 pseudomonas Q8tell pseudomonas Q8tell pseudomonas Q8tell pseudomonas Q8tell pseudomonas Q8tell chanosarc Q9bgx0 xylella fas Q8ter0 chlorobium 1 Q8264 rhizobium 1 Q8261 chizobium 1 Q8261 chizobium 0,9262 chizobium 0,9262 c   | odate) ; Thiotrichales; ; surface antigen in the databases. 7E CRC64; 72; Length 162;  | tches 0; Indels 0; Gaps 0; |
|--|--|----------------------------|
| Q985G4<br>Q9AGC7<br>Q8AGC7<br>Q8AGU7<br>Q8AGU7<br>Q92R89<br>Q92R13<br>Q91AS1<br>Q91AS1<br>Q91AS1<br>Q91AS1<br>Q91AS1<br>Q91AS1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q97EB1<br>Q9 | NARY; PRT; 162 AA.  rel. 16, Created)  rel. 16, Last sequence upda  rel. 16, Last annotation up  monis.  teria; Gammaproteobacteria;  piscirickettsia.  J., Thornton J.C., Kay W.W.  a genus-common Rickettsial  liscirickettsia salmonis.";  to the EMBL/GenBank/DDBJ  17661 MW; DDE99E6FD94A527  100.0%; Score 836; DB 2  100.0%; Pred. No. 3.1e-6   | 0; Mismatches              |
| 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0  |  | 41                         |
| 199<br>177<br>171<br>136<br>136<br>136<br>137<br>138<br>139<br>139<br>145<br>155<br>155<br>155<br>155<br>155<br>155<br>155<br>155<br>155   | (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16, (TremBlrel. 16, (TremBlrel. 16 | Conservative               |
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| 143<br>169<br>170<br>180<br>180<br>180<br>180<br>180<br>180<br>180<br>18   | KK8; AR-2AR-2AR-2AR-2AR-2AR-2AR-2AR-2AR-2AR-2  | Matches 162;               |
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                                                                                                                                                                                                                                                                                                                                                                                                                               26 SRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Rickettsia felis: molecular characterization of a new member of the spotted fever group.";
Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
EMBL; AF195118; AAG20452.1; -.
SEQUENCE 159 AA; 16497 MW; 34C5B020AF470A1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=21217364; PubMed=11321078;
Bouyer D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L.,
Zavala-Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98087556; PubMed=9425244;
MEDLINE=98087556; PubMed=9425244;
Bavis M.J., Ying Z., Brunner B.R., Pantoja A., Ferwerda F.H.;
"Rickettsial relative associated with papaya bunchy top disease.";
Curr. Microbiol. 36:80-84(1998).
                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=789;
                                                                                                                                                                                                                                                                                                          Length 148;
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Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                               148 AA; 15050 MW; A7AFEEFDE0AEEE4C CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                        5; DB 2;
L.8e-20;
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                                                                                                                                                                                                                                                                                                     Query Match 37.5%; Score 313.5;
Best Local Similarity 41.6%; Pred. No. 1.8e
Matches 57; Conservative 29; Mismatches
                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 kDa genus-common antigen.
Rickettsia felis (Rickettsia azadi).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                          17 kDa common-antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 EIYGTACROPDGRWQVI 158
                                                 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                    U76907; AAC02809.1; -.
                        PRELIMINARY;
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                                                                                                        Rickettsia sp.
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64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                             65 AVLGGQIGAGMDEQDRRLAELTSQRALEATPSGTSVEWRNPDNGNHGYVTPNKTY---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 -IKLNOSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAG 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Billings A.N., Teltow G.J., Walker D.H.;
"Molecular characterization of a novel spotted fever group rickettsial species from Ixodes scapularis in Texas.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF031534; AAB95267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Bertrand D., Hurst G.D.D., Majerus M.E.N.,
"On the evolution of male-killing: Monophyletic origin and horizontal
transfer of male-killing Rickettsia (a-Proteobacteria) from two con-
generic ladybirds, Adalia bipunctata L. and A. decempunctata L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 ONFSROEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK---
                                                                                                                                                                                                                                                                                                                                                                     17 kDa antigen (Fragment).
Rickettsia cooleyi.
Bacternia, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17kDA antigen (17 kDa antigen) (Fragment).
male-killing Rickettsia from Adalia bipunctata.
Bacteria, Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae, Rickettsieae; Rickettsia.
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ69518; CAB96383.1; -.
EMBL; AJZ69517; CAB96382.1; -.
NON TER 144 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 AA; 14215 MW; A27597A9AFD85FC3 CRC64;
                                                                                                                    120 QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVIS 159
                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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39.6%; Pred. No. 2.6e-16;
tive 23; Mismatches 49;
                                                                                                                                                                                                                                                               137 AA
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les 53; Conservative
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Matches

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RESULT 6 031065

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64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
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MEDLINE=93084757; PubMed=1452660;
MEDLINE=93084757; PubMed=1452660;
MEDLINE=91084767; PubMed=1452660;
MCDLINE=91084 M., Stenos J., Ross B.C., Stewart R.S., Dwyer B.
"Characterization and comparison of Australian human spotted fever group rickettsiae.";
                                                                                                                            MEDLINE=20575219; PubMed=11133455; Sloggett J.J., Webberley M.K., Schlienburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K., Bertrand D., Hurst G.D.D., Majerus M.E.N.; Incidence of male-kiling Rickettsia spp. (alpha-Proteobacteria) the Ten-Spot Ladybird Beetle Adalia decempunctata L. (Coleoptera: Appl. Environ. Microbiol. 67:270-277(2001).
                                                                                                                                                                                                                                                                                                                                                                                             9.
                                                                                                                                                                                                                                                                                                                                                     Score 259.5; DB 2; Length 144;
Pred. No. 1.2e-15;
2; Mismatches 48; Indels 9
                   male-killing Rickettsia from Adalia decempunctata.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales;
Rickettsiaceae, Rickettsieae, Rickettsia.
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.1%; Score 252; DB 2; Length 154; 35.5%; Pred. No. 6e-15; cive 29; Mismatches 57; Indels 1
                                                                                                                                                                                                                                                                                                    144 144
144 AA; 14801 MW; C825472F16A56AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 AA; 15849 MW; F5C35855EDB439D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
(Clone PRB FISF 1), 5' end CDS (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 QERROQYCREFQQKAMIAGQKQEIYGTACRQPDGR 154
                                                                                                                                                                                                                                                                                                                                         31.0%; Scor.
39.7%; Pred. No. 1...
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EMBL; M99391; AAA73386.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Best Local Similarity 39.7%,
Tranes 52; Conservative ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 35.5 es 55; Conservative
   kDa antigen (Fragment)
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132 KSYGNACRQPD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 EIYGTACRQPD 152
                                                                         NCBI_TaxID=120393;
                                                                                                                SEQUENCE FROM N.A.
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Q53154
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                                                                                                                                 10 NKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELT 69
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                                                                                                            26 SRQEVGAATGAVVGGVAGQLFCKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-99045882; PubMed-9828442;
Stenes J., Roux V., Walker D., Raoult D.;
Stenes J., Roux V., Walker D., Raoult D.;
Rickettaia honei sp. nov., the aetiological agent of Flinders Island
spotted fever in Australia.";
Int. J. Syst. Bacteriol. 48:1399-1404(1998).
EMBL; AF027124; AAB81846.1; -.
EMBL; AF060706; AAD20230.1; -.
                                                                           Gaps
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                                                                         6
                                      Length 144;
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                                                                       Indels
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Billings A.N., Yu X.-J., Teel P.D., Walker D.H.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
14785 MW; C8254739CCA56AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 137 AA; 14167 MW; 75BC1D0D745B428C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           031065; Q9WW02;
1-JAN-1998 (TERBLrel. 05, Created)
01-JAN-1998 (TERBLrel. 05, Last sequence update)
01-OCT-2002 (TERBLrel. 22, Last annotation update)
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Last sequence update)
Last annotation update)
                                  31.2%; Score 260.5; DB 2;
39.7%; Pred. No. 9.5e-16;
tive 22; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.0%; Score 259.5; DB 2; 39.7%; Pred. No. 1.1e-15; ive 22; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                           137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 kDa antigen (17 kDa protein) (Fragment). Rickettsia honei.
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NCBI_TaxID=37816;
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2002 (TrEMBLrel. 22,
                                                                       52; Conservative
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                                                                                                                                                                                                                                                           142 EIYGTACROPD 152
                                                                                                                                                                                                                                                                                            132 KAYGNACROPD 142
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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125 KAYGNACROPD 135
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 144 AA;
                                  Query Match
Best Local Similarity
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SEQUENCE
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Q9K4WB

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82 INQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ 141
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                        10 NKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELT 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=184231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 29.0%; Score 242.5; DB 2; Length 131; Local Similarity 38.6%; Pred. No. 3.5e-14; nes 49; Conservative 22; Mismatches 47; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 kDa protein (Fragment).
Rickettsia sp. California 2.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 AA; 13358 MW; D4152713C9FAA9CA CRC64;
                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Outer membrane protein (Fragment).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                 131 AA
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Emerg. Infect. Dis. 8:983-986(2002).
EMBL; AJ427882; CAD20878.1;
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                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                        142 EIYGTAC 148
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125 KAYGNAC 131
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Raoult D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=IrITA2;
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SEQUENCE
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Q8KLT5
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MEDLINE=22182650; PubMed=12194779;
Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.5%; Score 247; DB 2; Length 151; Best Local Similarity 36.2%; Pred. No. 1.6e-14; Matches 55; Conservative 26; Mismatches 57; Indels 14;
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Rickettsiaceae, Rickettsieae, Rickettsia.
NCBI_TaxID=35789;
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Rickettsiaceae; Rickettsiaae; Rickettsia.
NCBI_TaxID=184232;
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                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Nilsson K., Pahlson C.;
Nilsson K., Pahlson C.;
Novel peptide diagnostic reagent and kit for detection of rickettsiosis.";
Submitted (Aug. 1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF181036; AAG09427.1;
NON_TER 151
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                                                                                                                                01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Last annotation update)
125 QD-----CRVYTQTVVIGGKQQKAYGNACRQPDGQ 154
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01-OCT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
Outer membrane protein (Fragment).
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Emerg. Infect. Dis. 8:983-986(2002).
EMBL; AJ427883; CAD20879.1;
                                                                                                                                                                                           Outer membrane protein (Fragment). Rickettsia helvetica.
                                                                                             PRELIMINARY;
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Beninati T., Lo N.L., Noda H., Esposito F., Rizzoli A., Favia G.,
Genchi C.;
"First detection of spotted fever group rickettsiae in Ixodes ricinus
                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=35789;
                                                     (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22182650; PubMed=12194779;
                                                                                                                                      Outer membrane protein (Fragment).
17 KDA.
PRELIMINARY;
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125 KAYGNAC 131
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                                                                                                                                                                                                                                                                                                                                                                               STRAIN=IrITA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from Italy.";
                                                                                                                 01-MAR-2003
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Q9L522;
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EMBL; U04162; AAA19235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94117373; PubMed=8288533;
Werren J.H., Hurst G.D., Zhang W., Breeuwer J.A., Stouthamer R.,
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Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                      Query Match

28.4%; Score 237.5; DB 2; Length
Best Local Similarity 37.8%; Pred. No. 9.8e-14;
Matches 48; Conservative 22; Mismatches 48; Indels
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                                                                    SEQUENCE FROM N.A.
STRAIN=California 2;
Roux V., Raoult D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210693; AAG48554.1; -.
"A new SFG rickettsia isolated from fleas.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                   131 AA; 13374 MW; 23C8819B29FFF860 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
17 kDa antigen (Fragment).
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125 KAYGNAC 131
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SEQUENCE
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DE PLE REPRETATION OF SOLUTION

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82 LNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ 141
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Simezr J.A., Palmer A.T., Munderloh U.G., Kurtti T.J.;
Simezr J.A., palmer A.T., Munderloh U.G., Kurtti T.J.;
In a Rocky Mountain wood tick, Dermacentor andersoni, cell line.";
Appl. Environ. Microbiol. 67:546-552(2001).
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01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
17 Aba surface antigen (Fragment).
Rickettsia peacockii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiaceae; Rickettsiaceae; Rickettsiaee;
                                                                                                                                                                                                          / Match 28.3%; Score 236.5; DB 2; Length 131; Local Similarity 37.8%; Pred. No. 1.2e-13; ne 48; Conservative 22; Mismatches 48; Indels 9.
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                                                                                                                                   131 AA; 13383 MW; D78C171050CAA9CA CRC64;
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EMBL; AJ427881; CAD20877.1; -.
NON TER 1
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RESULT :

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        Db
        10 NKQGTGTLLGGAGGALLGSQFGKGKQLVGVGYGALLGAVLGGQIGAGMDEQDRRLAELT 69

        QY
        82 LNQSLEKVKAGQVTRWRNPDTGNSYSVEPVTYQRYNKQERRQQYCREFQQKAMIAGQKQ 141

        Db
        70 SQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY-----RNSTGQYCREYTQTVVIGGKQQ 124

        QY
        142 EIYGTAC 148

        Bb
        125 KAYGNAC 131
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Search completed: November 5, 2003, 20:15:03 Job time: 25.7824 secs